

Linkage Map of *Escherichia coli* K-12, Edition 8†

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INTRODUCTION

This edition of the linkage map is based on the experimental literature from July 1982 through June 1988, on personal communications received during that period or received in response to questions asked during the preparation of the map, and on the literature cited in previous editions of the map. The positions of 1,403 loci are shown in Fig. 1. About 400 new genes have been added in this edition of the map, and a few loci have been removed, either because they were shown to be identical to other loci on the map or because their existence could not be confirmed. The genes included in the map are listed alphabetically in Table 1 with their map positions and functions.

It must be emphasized that these reviews of the linkage data are intended to serve as guides to the literature and not as a substitute for consulting the original research papers. The present map (Fig. 1) is based on data that vary widely in precision, and some map positions are compromises based on contradictory data. Obviously, it is not possible to discuss each of these problems in detail in this review.

All of the literature citations in previous editions of the map (43, 45, 46) can be found in the reprinting of map edition 7 which is included in the comprehensive two-volume review of the cellular and molecular biology of *Escherichia coli* and *Salmonella typhimurium* which was published in 1987 (44).

† A limited supply of the following will be available from ASM: reprints of this article and wall charts (ca. 21 × 24 1/2") of the *E. coli* linkage map. Shipped together in a mailing tube. \$10.50, U.S. and Canada; \$12.50, foreign (surface). Prices are subject to change without notice. All orders must be accompanied by payment in U.S. dollars, drawn on a U.S. bank located within the continental United States, or charged to MasterCard, VISA, or American Express. ASM does not accept wire transfers. Charge card orders may be placed by telephone (202-737-3600) or by fax (202-737-0368). Mail orders should be addressed to: American Society for Microbiology, Publication Sales, 1325 Massachusetts Ave., N.W., Washington, DC 20005-4171.

MAP UNITS

The basic units of the linkage map as drawn in Fig. 1 are still minutes, as determined by time of entry of markers in interrupted conjugation experiments (46). In the 1983 map (43), the entire linkage group was linked by cotransduction data for the first time. Many small regions had been studied in fine detail by restriction mapping and sequencing, and the distances between many loci had been determined in kilobases of DNA.

Since 1983, restriction maps of the *E. coli* chromosome have been produced (584, 1021), and one of these has now been completed to give a physical map of the entire genome (577, 578, 584). Unfortunately, the source of the DNA used in constructing the physical map was strain W3110 (584), which carries an inversion of around 19% of the chromosome. However, the exact endpoints of this inversion have now been determined, and the small gaps in the original restriction map have been closed (577, 578, 587). According to this map, the chromosome comprises 4,750 kilobase pairs (kb) of DNA.

In this edition of the linkage map, I have used the time-of-entry map as a framework, except for the region between the *his* operon and *gyrA*, for which the conjugational and transduational data have been contradictory in the past. Cotransduction data have been converted to map units as described in previous editions of the map, assuming that bacteriophage P1 brings in effectively approximately 2 min of DNA. In converting cotransduction, restriction, and sequencing data into map units, I have assumed that 1 min corresponds to 47.5 kb.

NOMENCLATURE

The system of nomenclature used in this edition of the map is that of Demerec et al. (268), with modifications as discussed in previous editions. The assignment of gene symbols is coordinated by the *E. coli* Genetic Stock Center and the *Salmonella* Genetic Stock Center, in an effort to

avoid the assignment of the same gene symbol to two different genes or the assignment of different gene symbols to genes that are homologous in the two organisms. Allele number assignments are also coordinated by the two stock centers (959). It is important that each mutation be assigned a unique allele number so that it can be recognized in any strain in which it is found. This applies to transposon insertions not in known genes and to deletions as well as to point mutations.

The cumbersome and disparate nomenclatures for the genes affecting flagellar structure and function in *E. coli* and *S. typhimurium* have been revised and brought into agreement by Iino et al. (504), and their proposed uniform nomenclature has been adopted in this edition of the map.

Modifications to the nomenclature for the often duplicated and/or tandemly repeated tRNA genes have been proposed by Fournier and Ozeki (341) and adopted in this edition.

A new convention has been adopted for the loci involved in the termination of replication (267, 343, 460, 463–465, 842) and for a set of repetitive sequences responsible for duplications in the chromosome (652, 944), since these loci do not fit the classical definition of a gene. These loci are being designated *TerA*, *TerB*, etc., and *RhsA*, *RhsB*, etc., respectively. The symbols are italicized but the first letter is capitalized, which should serve to distinguish them from the symbols for genes, gene products, or phenotypes.

The numerous members of the family of dispersed repetitive extragenic palindromic sequences, called P.U.S. or REPS (73, 378), informally, have not been included in this review.

The designations of two genes (*bglC* and *bglS*) in the *bgl* operon at 84 min have been changed to *bglG* and *bglF*, respectively. When it was discovered that the gene coding for β-glucoside transport (*bglC*) is the second gene in the operon and that the positive regulatory gene (*bglS*) is the first gene, rather than the reverse as had been thought previously, the designations for the genes with these two functions were switched, rather than switching the gene order on the map (685, 973). In the hope of preventing confusion about the function affected in mutants isolated before this switch occurred, the designations of these two genes have been changed.

Gene symbols used formerly or proposed as alternatives for those used in Table 1 are listed in Table 2 beside the symbols used in Table 1 for the corresponding loci.

COMMENTS ON THE MAP

0 to 10 min. The locus *arl* has been removed from the map at 2 min because its presence could not be verified (449; J. B. Hayes, personal communication). In the 8-min region, the nucleotide sequence of one end of the hybridization loop of DNA (showing no homology to *S. typhimurium*) which contains the *lac* operon has been determined (159). A sequence similar to sequences shown to be involved in site-specific recombination was identified at or near the junction of the loop with homologous DNA. The 6- to 8-min region is noted for a comparatively high frequency of formation of deletions and inversions.

10 to 20 min. Efforts to confirm the existence of the *minA* gene at 10 min have failed (253). This locus has been removed from the map.

20 to 30 min. The *capS* mutants have apparently been lost (A. Markovitz, personal communication). This locus has been removed from the map at approximately 23 min. The *chlF* mutant has also been lost (J. DeMoss, personal communication), and this locus has been removed from the map at approximately 27 min. Efforts to confirm the existence of the *aroT* locus at 28 min have failed, and there are no mutants, so this marker, too, has been removed from the map.

30 to 40 min. The once mysterious region including the “terminus of replication” is now one of the most intensively studied regions of the map (34, 43, 79). The nature of the terminus region is now quite different from the concept held in 1983 (267, 343, 460, 463–465, 832). The *terC* gene has been removed from the map and replaced by four *Ter* loci.

40 to 50 min. The *aspV* locus was placed at 43 min in error (H. Ozeki, personal communication) and has now been removed. The symbol *aspV* has been reassigned to the asparaginyl tRNA₁ gene at 5.1 min. There is now general agreement on the order of the loci in the *his-gyrA* region, although the precise reasons for the previous contradictory data have not been determined (736). It is still possible that the length and orientation of part of this region are not the same in all of the strains used in earlier mapping studies. In the 1983 map (43) the length of this interval was 4.3 min. Recent cotransduction data confirm this length, which is about 1 min less than that suggested by the physical map (584).

50 to 60 min. The strains described as carrying mutations at the loci *nirE* at 50 min and *nirF* at 53 min have been shown to have normal nitrate reductase activity (680). These loci have been removed from the map. The existence of the *pfkC* locus is very doubtful (D. Fraenkel, personal communication), and it has been removed from the map.

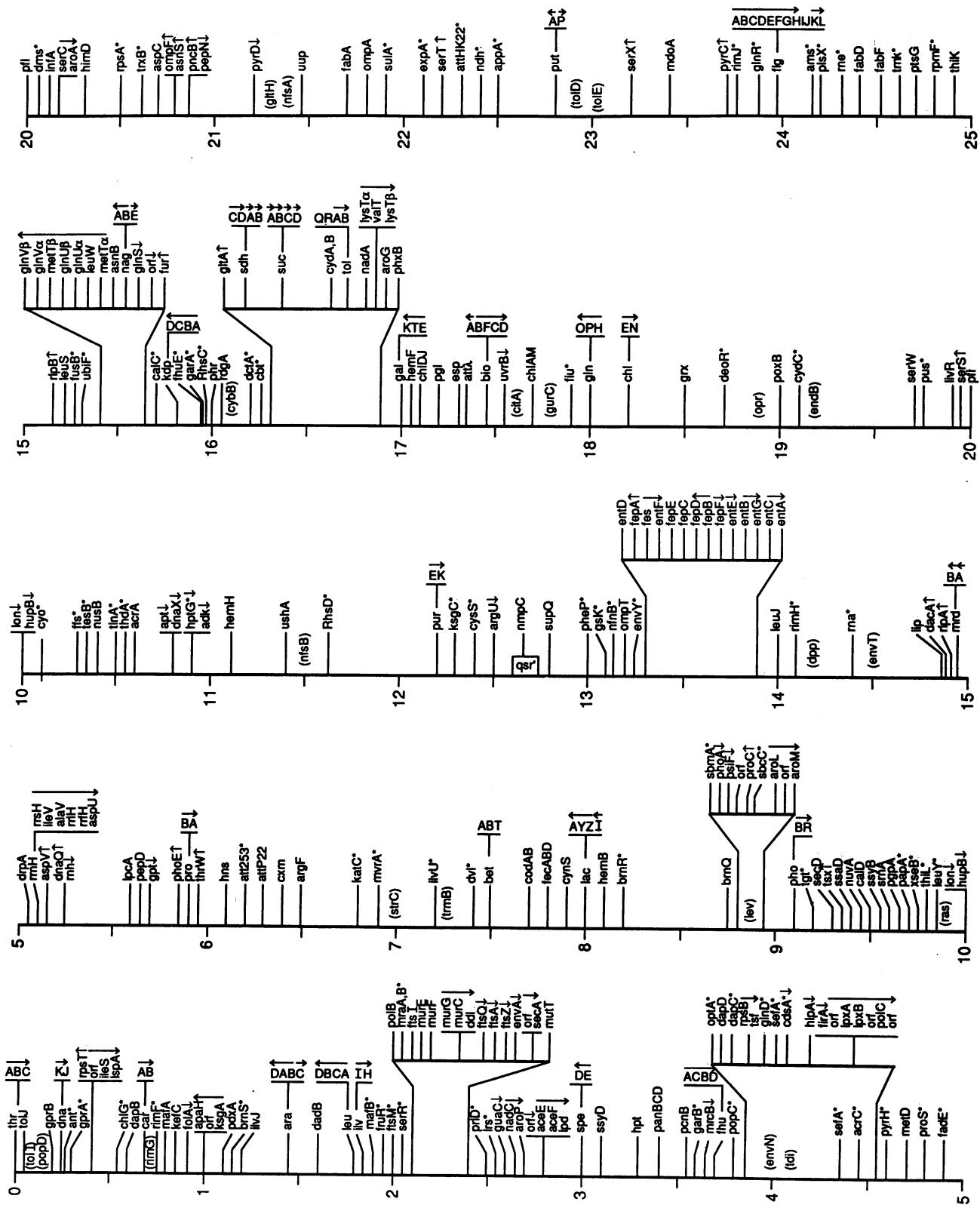
60 to 70 min. The locus *kpsA* should not have been placed on the map, since the *kps* genes do not exist in *E. coli* K-12. This locus has been removed from the map.

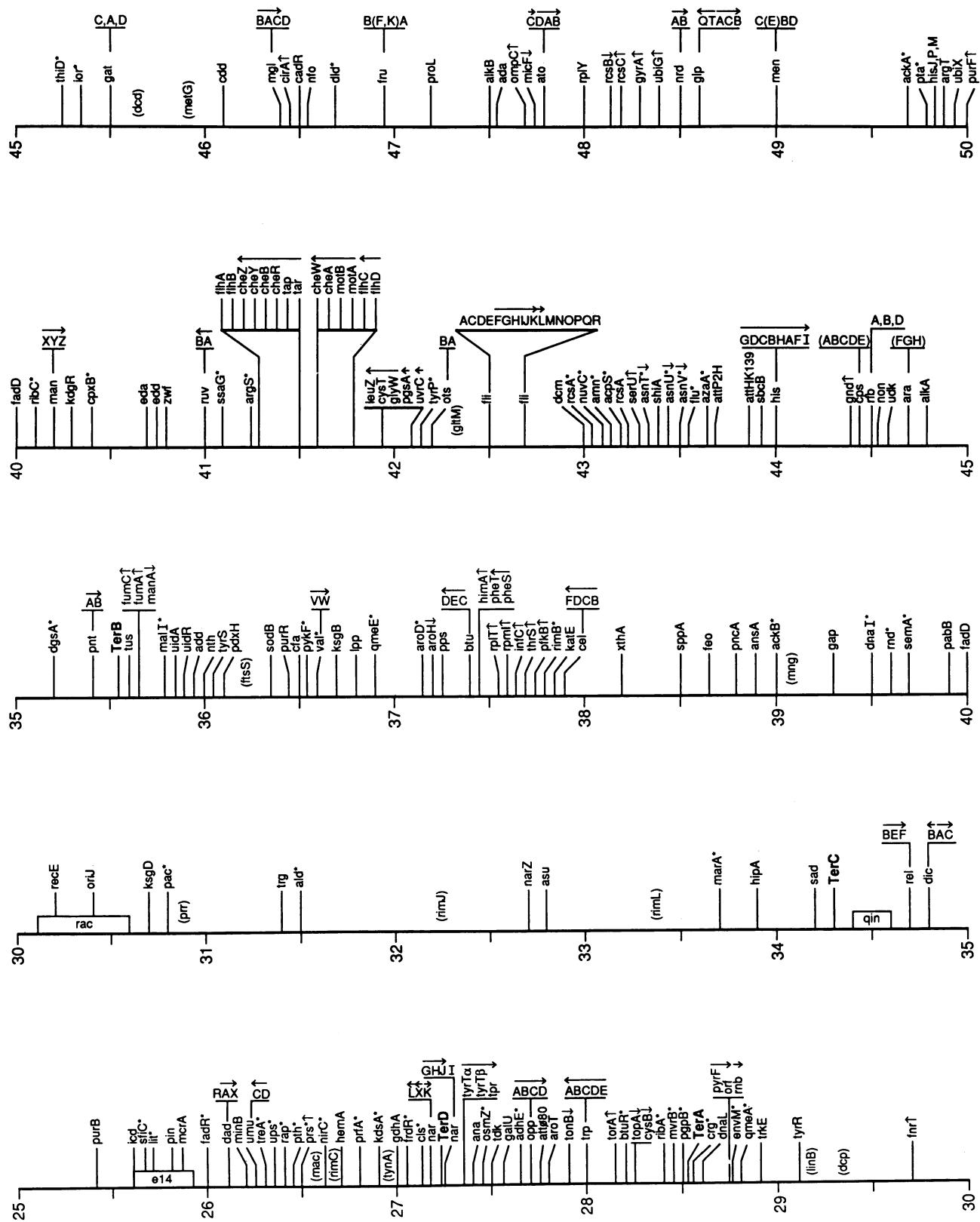
80 to 90 min. In constructing a physical and genetic map of the *ilv-metE* region, Aldea et al. (14) found the length of this region to be about 1.2 min, whereas the physical map of Kohara et al. (584) suggests a distance of about 1.1 min. The length of this region was shown as 0.9 min in the 1983 map (43). These authors devised a new formula for converting cotransduction frequencies to map distance in order to account for these discrepancies. Analysis of all data available gives a length of 1.3 min in my hands, as shown in Fig. 1.

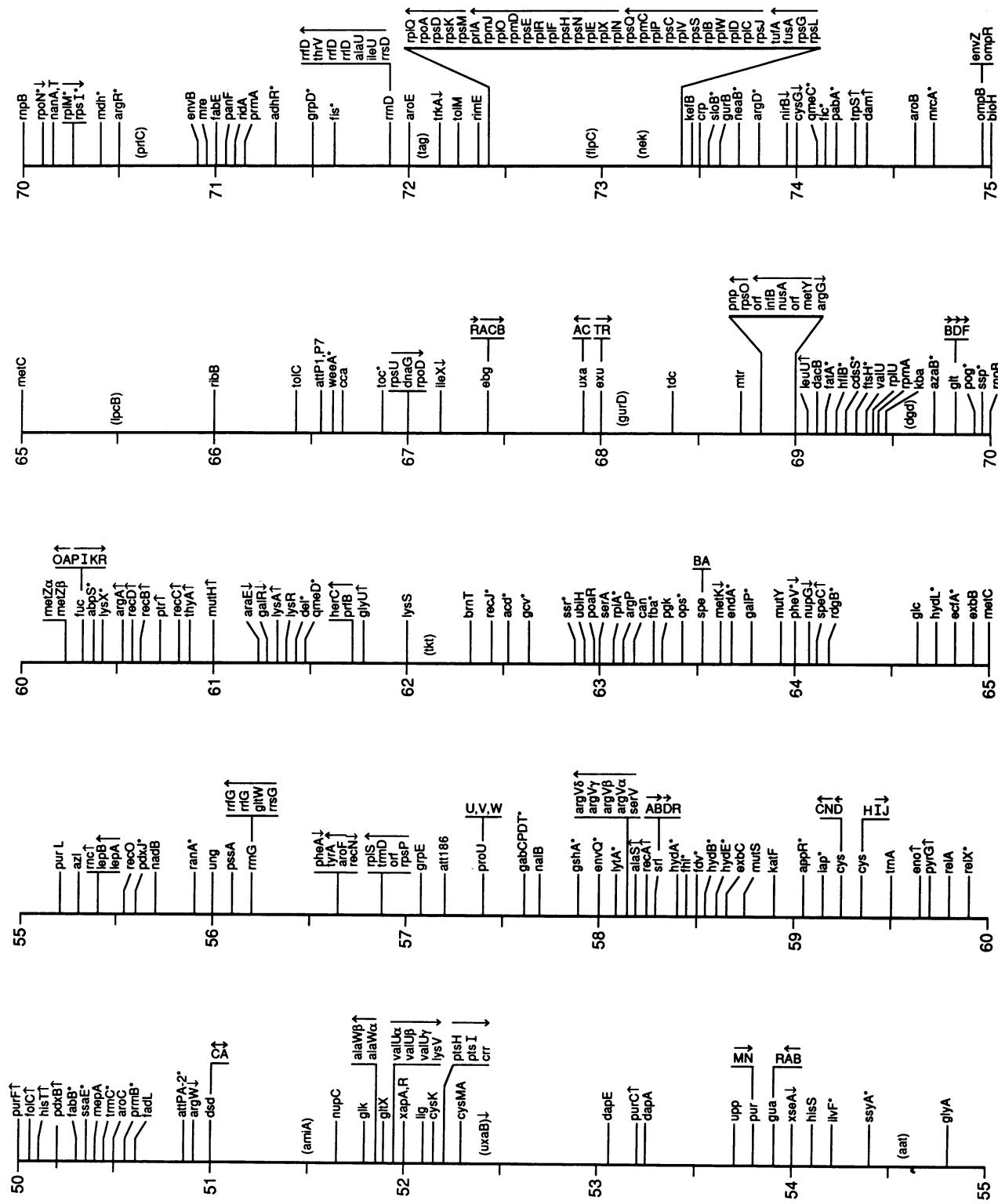
The *dnaP* mutant has been shown to carry a *dnaG* mutation (765), and a second mutation conferring temperature sensitivity could not be found in the strain (T. Yura, personal communication). The *dnaP* locus has been removed from the map at 85 min.

90 to 100 min. There is some uncertainty about the order of genes in the region between the *malB* operon and *uvrA*,

FIG. 1. Linear scale drawings representing the circular linkage map of *E. coli* K-12. The time scale of 100 min, beginning arbitrarily with zero at the *thr* locus, is based on the results of interrupted conjugation experiments. The genetic symbols are defined in Table 1. Parentheses around a gene symbol indicate that the position of that marker is not well known and may have been determined only within 5 to 10 min. An asterisk indicates that a marker has been mapped more precisely but that its position with respect to nearby markers is not known. Arrows above genes and operons indicate the direction of transcription of these loci.







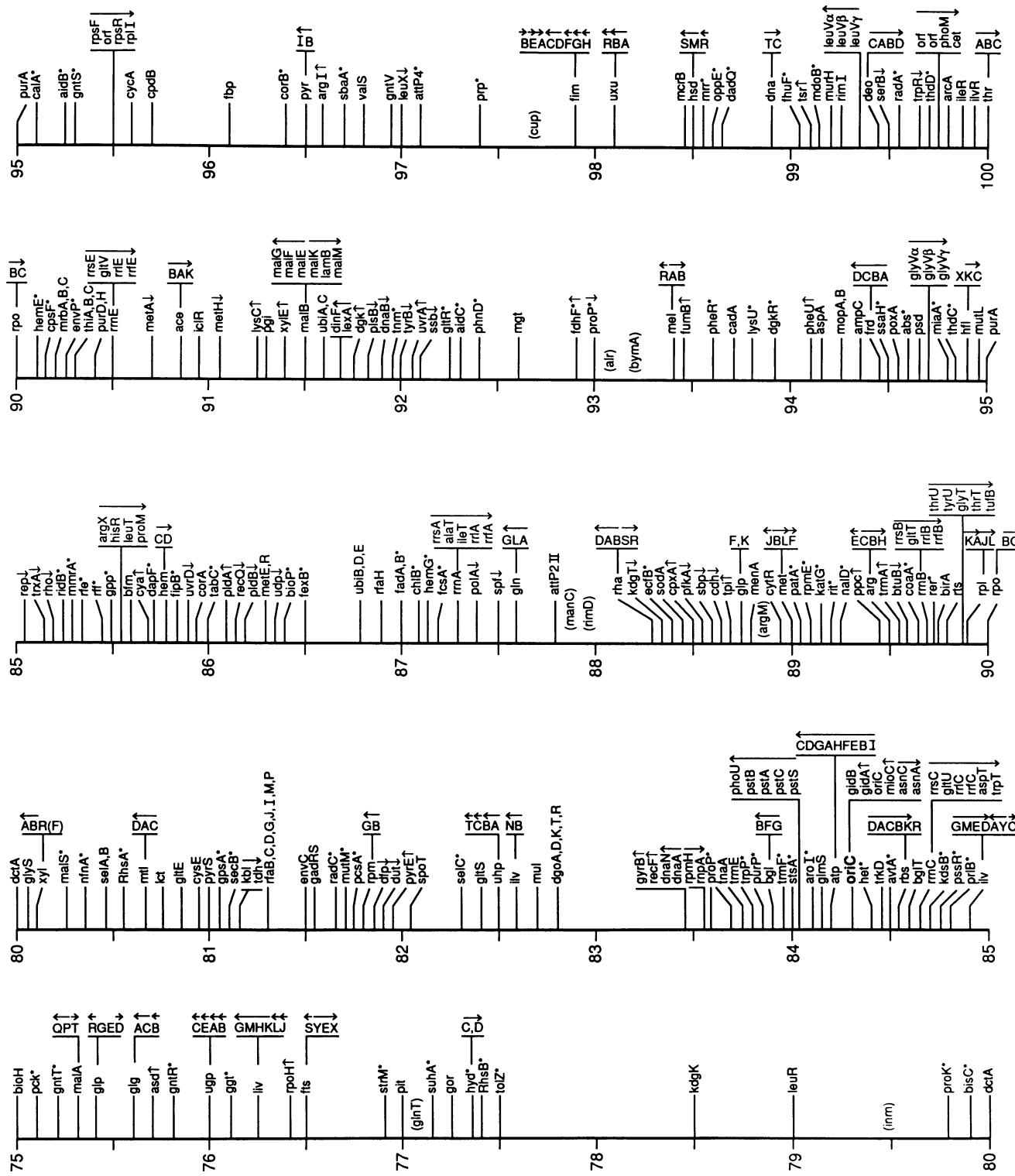


TABLE 1. Genetic markers of *E. coli* K-12

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>aat</i>		(55)	Aminoacyl-tRNA-protein-transferase (EC 2.3.2.6)	B
<i>abpS</i>		60	Low-affinity transport system for arginine and ornithine; periplasmic binding protein	180
<i>abs</i>		95	Sensitivity and permeability to antibiotics and dyes	195
<i>acd</i>		63	Acetaldehyde-CoA dehydrogenase	C
<i>aceA</i>	Acetate	91	<i>icl</i> ; utilization of acetate; isocitrate lyase (EC 4.1.3.1)	A, C, 910
<i>aceB</i>	Acetate	91	<i>mas</i> ; utilization of acetate; malate synthase A (EC 4.1.3.2)	A, C
<i>aceE</i>	Acetate	3	<i>aceEl</i> ; acetate requirement; pyruvate dehydrogenase (decarboxylase component)	A, B, C, 422, 739, 1029
<i>aceF</i>	Acetate	3	<i>aceE2</i> ; acetate requirement; pyruvate dehydrogenase (di-hydrolipoylethanol acyltransferase component)	A, B, C, 422, 1029, 1043
<i>aceK</i>		91	Isocitrate dehydrogenase kinase/phosphatase	194, 220, 576, 615, 616
<i>ackA</i>		50	Acetate kinase (EC 2.7.2.1) activity	B, C
<i>ackB</i>		39	Acetate kinase (EC 2.7.2.1) activity	C
<i>acpS</i>		43	CoA:apo-[acyl-carrier protein] pantetheinephosphotransferase (EC 2.7.8.7); holo-[acyl-carrier protein] synthase	C
<i>acrA</i>	Acridine	11	<i>lir</i> , <i>Mb</i> , <i>mbl</i> , <i>mtc</i> ; sensitivity to acriflavine, phenethyl alcohol, and sodium dodecyl sulfate	A, C
<i>acrC</i>	Acridine	4	Sensitivity to acriflavine	C
<i>ada</i>		48	Inducible DNA repair system protecting against methylating and alkylating agents; <i>O</i> ⁶ -methylguanine-DNA methyltransferase	C, 560, 635, 703, 744, 772, 1087, W
<i>add</i>		36	Adenosine deaminase (EC 3.5.4.4)	B
<i>adhE</i>		27	CoA-linked acetaldehyde dehydrogenase and alcohol dehydrogenase	B, C, 232
<i>adhR</i>		71	Regulatory gene for <i>acd</i> and <i>adhE</i>	196, 191, F
<i>adk</i>		11	<i>dnaW</i> ; <i>plsA</i> ; adenylate kinase (EC 2.7.4.3) activity; pleiotropic effects on glycerol-3-phosphate acyltransferase activity	A, B, C, 147
<i>aidB</i>		95	Induced by alkylating agents	1145, T
<i>aidC</i>		92	Induced by alkylating agents	1145
<i>alaS</i>	Alanine	58	<i>ala-act</i> ; alanyl-tRNA synthetase (EC 6.1.1.7)	A, B, C
<i>alaT</i>	Alanine	87	<i>talA</i> ; alanine tRNA 1B; in <i>rrnA</i> operon	B, 587
<i>alaU</i>	Alanine	72	<i>talD</i> ; alanine tRNA 1B; in <i>rrnD</i> operon	B, 587
<i>alaV</i>	Alanine	5	Alanine tRNA 1B in <i>rrnH</i> operon	C, 587
<i>alaW</i>	Alanine	52	Alanine tRNA 2 (tandemly duplicated gene)	587
<i>ald</i>		31	Aldehyde dehydrogenase, NAD-linked	189
<i>alkA</i>	Alkylation	45	<i>aidA</i> ; 3-methyladenine DNA glycosylase II, inducible	B, C, 199, 773, 774, 1087, 1145
<i>alkB</i>	Alkylation	47	<i>aidD</i> ; DNA repair system specific for alkylated DNA	560, 561, 1145
<i>alr</i>		(93)	Alanine racemase (EC 5.1.1.1)	A
<i>amiA</i>		(51)	N-Acetylumuramyl-L-alanine amidase activity	1104
<i>amn</i>		43	AMP nucleosidase (EC 3.2.2.4)	636
<i>ampC</i>	Ampicillin	94	β-Lactamase; penicillin resistance	A, B, C, 525
<i>ams</i>		24	Alteration of mRNA stability	C, 183
<i>ana</i>		27	Alcohol dehydrogenase (EC 1.1.1.1) and acetaldehyde dehydrogenase (EC 1.2.1.10) activity	B, C
<i>ansA</i>		39	L-asparaginase I, cytoplasmic	C, 1033
<i>ant</i>		0	Na ⁺ /H antiporter activity	381
<i>apaH</i>		1	Diadenosine tetraphosphatase	101, 729
<i>appA</i>		22	pH 2.5 acid phosphatase; exopolyphosphatase (EC 3.6.1.11)	117, 250
<i>appR</i>		59	Expression of pH 2.5 acid phosphatase	1110
<i>apt</i>		11	Adenine phosphoribosyltransferase (EC 2.4.2.7)	B, 457, 458
<i>araA</i>	Arabinose	1	L-Arabinose isomerase (EC 5.3.1.4)	A, B, 630
<i>araB</i>	Arabinose	1	Ribulokinase (EC 2.7.1.16)	A, B, C, 293, 630
<i>araC</i>	Arabinose	1	Regulatory gene; activator and repressor protein	A, B, C, 293
<i>araD</i>	Arabinose	1	L-Ribulosephosphate 4-epimerase (EC 5.1.3.4)	A, B, 630
<i>araE</i>	Arabinose	61	Low-affinity L-arabinose transport system; L-arabinose proton symport	A, C, 688, 1052
<i>araF</i>	Arabinose	45	L-Arabinose-binding protein	B, C, 982, 983
<i>araG</i>	Arabinose	45	High-affinity L-arabinose transport system	C, 983
<i>araH</i>	Arabinose	45	High-affinity L-arabinose transport system; membrane protein	983
<i>arcA</i>		100	<i>dye</i> , <i>fexA</i> , <i>msp</i> , <i>seg</i> , <i>sfrA</i> ; negative regulatory gene of genes in aerobic pathways	A, B, C, 160, 161, 286, 519

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>argA</i>	Arginine	61	<i>argB</i> , <i>Argl</i> , <i>Arg2</i> ; amino acid acetyltransferase; <i>N</i> -acetylglucosamine synthase (EC 2.3.1.1)	A, B, C, 142, 296, 796, 965
<i>argB</i>	Arginine	90	<i>argC</i> ; acetylglutamate kinase (EC 2.7.2.8)	A, B, C
<i>argC</i>	Arginine	90	<i>argH</i> , <i>Arg2</i> ; <i>N</i> -acetyl- γ -glutamyl-phosphate reductase (EC 1.2.1.38)	A, B, C, 88, 854
<i>argD</i>	Arginine	74	<i>argG</i> , <i>Argl</i> ; acetylornithine δ -aminotransferase (EC 2.6.1.11)	A, 911
<i>argE</i>	Arginine	90	<i>argA</i> , <i>Arg4</i> ; acetylornithine deacetylase (EC 3.5.1.16)	A, B, C, 88, 854
<i>argF</i>	Arginine	7	<i>argD</i> , <i>Arg5</i> ; ornithine carbamoyltransferase (EC 2.1.3.3) (duplicate gene)	A, B, C, 855, 1141
<i>argG</i>	Arginine	69	<i>argE</i> , <i>Arg6</i> ; argininosuccinate synthetase (EC 6.3.4.5)	A
<i>argH</i>	Arginine	90	<i>argF</i> , <i>Arg7</i> ; argininosuccinate lyase (EC 4.3.2.1)	A, B, C
<i>argI</i>	Arginine	97	Ornithine carbamoyltransferase (EC 2.1.3.3) (duplicate gene)	A, B, 86, 855, 921
<i>argM</i>	Arginine	(89)	Acetylornithine transaminase; cryptic gene; may be duplicate of <i>argD</i>	911
<i>argP</i>	Arginine	63	Transport of arginine, ornithine, and lysine	A
<i>argR</i>	Arginine	71	<i>Rarg</i> ; regulatory gene; repressor of <i>arg</i> regulon	A, C, 651
<i>argS</i>	Arginine	(40)	Arginyl-tRNA synthetase (EC 6.1.1.19)	A, 793
<i>argT</i>	Arginine	50	Sequence homologous to <i>argT</i> of <i>S. typhimurium</i> , which codes for lysine-, arginine-, ornithine-binding protein	807
<i>argU</i>	Arginine	13	<i>dnaY</i> , <i>pin</i> ; arginine tRNA 4	B, C, 341, 359, 373, 587
<i>argV</i>	Arginine	58	Arginine tRNA 2 (tandemly quadruplicated gene)	341
<i>argW</i>	Arginine	51	Arginine tRNA 5	587
<i>argX</i>	Arginine	85	Arginine tRNA 3	485, 587
<i>aroA</i>	Aromatic	20	3-enol-pyruvoylshikimate-5-phosphate synthase (EC 2.5.1.19)	A, 291, 292
<i>aroB</i>	Aromatic	75	Dehydroquinate synthase (EC 4.6.1.3)	A, 740
<i>aroC</i>	Aromatic	51	Chorismate synthase (EC 4.6.1.4)	A
<i>aroD</i>	Aromatic	37	3-Dehydroquinate dehydratase (EC 4.2.1.10)	A, C, 118
<i>aroE</i>	Aromatic	72	Dehydroshikimate reductase (EC 1.1.1.25)	A, 24, 730
<i>aroF</i>	Aromatic	57	DAHP synthetase (tyrosine repressible)	A, 488, 1008
<i>aroG</i>	Aromatic	17	DAHP synthetase (phenylalanine repressible)	A, C, 254
<i>aroH</i>	Aromatic	37	DAHP synthetase (tryptophan repressible)	A, C, 118, 290
<i>aroI</i>	Aromatic	84	Function unknown	A
<i>aroL</i>	Aromatic	9	Shikimate kinase II (EC 2.7.1.71)	B, 261, 262
<i>aroM</i>	Aromatic	9	Unknown function; regulated by <i>aroR</i>	261, 262
<i>aroP</i>	Aromatic	3	General aromatic amino acid transport	A, C, 422, 912
<i>aroT</i>	Aromatic	28	<i>aroR</i> , <i>trpR</i> ; transport of aromatic amino acids, alanine, and glycine	A, B
<i>asd</i>		76	<i>dap</i> + <i>hom</i> ; aspartate semialdehyde dehydrogenase (EC 1.2.1.11)	A, C
<i>asnA</i>	Asparagine	84	Asparagine synthetase A (EC 6.3.1.1)	A, B, C, 152
<i>asnB</i>	Asparagine	16	Asparagine synthetase B (EC 6.3.1.1)	B, C, 864
<i>asnC</i>	Asparagine	84	Regulatory gene	277
<i>asnS</i>	Asparagine	21	<i>lcs</i> ; asparaginyl-tRNA synthetase (EC 6.1.1.22)	B, C, 506
<i>asnT</i>	Asparagine	43	Asparagine tRNA	B, C, 341, 587
<i>asnU</i>	Asparagine	43	Asparagine tRNA	587
<i>asnV</i>	Asparagine	43	Asparagine tRNA	587
<i>aspA</i>	Aspartate	94	L-Aspartate ammonia-lyase (aspartase) (EC 4.3.1.1)	A, B, 423
<i>aspC</i>	Aspartate	21	Aspartate aminotransferase (EC 2.6.1.1)	B, 340, 607, 697
<i>aspT</i>	Aspartate	85	<i>tasC</i> ; aspartate tRNA 1, triplicate gene; in <i>rrnC</i> operon	B, C, 587
<i>aspU</i>	Aspartate	5	Aspartate tRNA 1, triplicate gene; in <i>rrnH</i> operon	C, 587
<i>aspV</i>	Aspartate	5	Aspartate tRNA 1, triplicate gene	C, 477, 587
<i>asu</i>		33	Asparagine utilization, as sole nitrogen source	191
<i>atoA</i>	Acetoacetate	48	Acetyl-CoA:acetoacetyl-CoA transferase (EC 2.8.3.-) β -subunit	A, 588
<i>atoB</i>	Acetoacetate	48	Acetyl-CoA acetyltransferase (EC 2.3.1.9)	A, 528
<i>atoC</i>	Acetoacetate	48	Positive regulatory gene	A, 528, 529
<i>atoD</i>	Acetoacetate	48	Acetyl-CoA:acetoacetyl-CoA transferase (EC 2.8.3.-) β -subunit?	528
<i>atpA</i>	ATP	84	<i>papA</i> , <i>uncA</i> ; membrane-bound ATP synthase (EC 3.6.1.3), F ₁ sector, α -subunit	A, B, C, 578, 1152
<i>atpB</i>	ATP	84	<i>papD</i> , <i>uncB</i> ; membrane-bound ATP synthase (EC 3.6.1.3), F ₀ sector, subunit a	A, B, C, 801, 1146, 1152

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>atpC</i>	ATP	84	<i>papG, uncC</i> ; membrane-bound ATP synthase (EC 3.6.1.3), F ₁ sector, ε-subunit	B, C, 1152
<i>atpD</i>	ATP	84	<i>papB, uncD</i> ; membrane-bound ATP synthase (EC 3.6.1.3), F ₁ sector, β-subunit	B, C, 1152
<i>atpE</i>	ATP	84	<i>papH, uncE</i> ; membrane-bound ATP synthase (EC 3.6.1.3), F ₀ sector, subunit c; DCCD-binding protein	B, C, 722, 1152
<i>atpF</i>	ATP	84	<i>uncF</i> ; membrane-bound ATP synthase (EC 3.6.1.3), F ₀ sector, subunit b	C, 1152
<i>atpG</i>	ATP	84	<i>papC, uncG</i> ; membrane-bound ATP synthase (EC 3.6.1.3), F ₁ sector, γ-subunit	B, C, 578, 1152
<i>atpH</i>	ATP	84	<i>papE, uncH</i> ; membrane-bound ATP synthase (EC 3.6.1.3), F ₁ sector, δ-subunit	C, 1152
<i>atpI</i>	ATP	84	<i>uncI</i> ; membrane-bound ATP synthase (EC 3.6.1.3), subunit ?	148, 537, 801, 872, 1146, 1152
<i>attE14</i>	Attachment	26	Attachment site for element E14	C
<i>attHK22</i>	Attachment	22	<i>atthtt</i> ; attachment site for phage HK022	C
<i>attHK139</i>	Attachment	44	Attachment site for phage HK139	C
<i>attλ</i>	Attachment	17	Integration site for prophages λ, 82, and 434	A, B, C
<i>attP1, P7</i>	Attachment	67	<i>loxB</i> ; integration site for phages P1 and P7	C
<i>attP2H</i>	Attachment	44	Phage P2 integration site H	A
<i>attP2II</i>	Attachment	88	Phage P2 integration site II	A
<i>attP4</i>	Attachment	97	Integration site for phage P4	C
<i>attP22</i>	Attachment	6	<i>ata</i> ; integration site for phage P22	A
<i>attPA-2</i>	Attachment	51	Integration site for phage PA-2	B
<i>attΦ80</i>	Attachment	28	Integration site for prophage Φ80	A, B
<i>attI86</i>	Attachment	57	Integration site for prophage I86	A
<i>att253</i>	Attachment	6	Integration site for phage 253	871
<i>avtA</i>		84	Alanine-α-ketoisovalerate transaminase, transaminase	C
<i>azaA</i>	Azaserine	44	Resistance or sensitivity to azaserine	C
<i>azaB</i>	Azaserine	70	Resistance or sensitivity to azaserine	C
<i>azl</i>	Azaleucine	55	Regulation of <i>ilv</i> and <i>leu</i> genes; azaleucine resistance	A
<i>betA</i>	Betaine	7	Choline dehydrogenase	21, 1058
<i>betB</i>	Betaine	7	Betaine aldehyde dehydrogenase	21
<i>betT</i>	Betaine	7	High-affinity choline transport	21
<i>bfm</i>		86	Phage BF23 multiplication	A
<i>bglA</i>	β-Glucoside	84	<i>bglD</i> ; phospho-β-glucosidase A	A, B
<i>bglB</i>	β-Glucoside	84	<i>bglA</i> ; phospho-β-glucosidase B	A, B, C, 685, 973
<i>bglF</i>	β-Glucoside	84	<i>bglB, bglC</i> ; β-glucoside transport	A, B, C, 128, 685
<i>bglG</i>	β-Glucoside	84	<i>bglC, bglS</i> ; positive regulatory gene	A, 685, 904, 905, 973
<i>bglT</i>	β-Glucoside	85	<i>bglE</i> ; regulatory gene for phospho-β-glucosidase A synthesis	A
<i>bioA</i>	Biotin	17	7,8-Diaminopelargonic acid synthetase	A, B, C, 1072
<i>bioB</i>	Biotin	17	Biotin synthetase	A, B, C, 1072
<i>bioC</i>	Biotin	17	Block prior to pimeloyl CoA	A, B, 1072
<i>bioD</i>	Biotin	17	Dethiobiotin synthetase	A, B, 1072
<i>bioF</i>	Biotin	17	7-Keto-8-aminopelargonic acid synthetase	A, B, 1072
<i>bioH</i>	Biotin	75	<i>bioB</i> ; block prior to pimeloyl CoA	A, C
<i>bioP</i>	Biotin	86	<i>birB</i> ; biotin transport	A, B, C
<i>birA</i>	Biotin retention	90	<i>birR, dhhB</i> ; biotin-[acetyl-CoA carboxylase] holoenzyme synthetase; biotin operon repressor	A, B, C, 483
<i>bisC</i>	Biotin sulfoxide	80	Biotin sulfoxide reductase, structural gene	B, C
<i>brnQ</i>	Branched chain	9	Transport system 1 for isoleucine, leucine, and valine	A, B
<i>brnR</i>	Branched chain	8	Component of transport systems 1 and 2 for isoleucine, leucine, and valine	A
<i>brnS</i>	Branched chain	1	Transport system for isoleucine, leucine, and valine	A
<i>brnT</i>	Branched chain	62	Low-affinity transport system for isoleucine	B
<i>btuB</i>	B ₁₂ uptake	90	<i>bfe, btuA, cer</i> ; receptor for vitamin B ₁₂ , E colicins, and phage BF23	A, B, C, 40, 41, 455
<i>btuC</i>	B ₁₂ uptake	37	Vitamin B ₁₂ transport	B, 274, 276, 351
<i>btuD</i>	B ₁₂ uptake	37	Vitamin B ₁₂ transport, membrane-associated protein	274, 276, 351
<i>btuE</i>	B ₁₂ uptake	37	Vitamin B ₁₂ transport, periplasmic protein?	274, 351
<i>btuR</i>	B ₁₂ uptake	28	Regulatory gene affecting <i>btuB</i>	674
<i>bymA</i>		(93)	Bypass of maltose permease at <i>malB</i>	A
<i>cadA</i>	Cadaverine	94	Lysine decarboxylase (EC 4.1.1.18)	C
<i>cadR</i>	Cadaverine	46	<i>lysP?</i> ; regulatory gene for lysine decarboxylase	C, W
<i>calA</i>	Calcium	95	Calcium transport	C

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>calC</i>	Calcium	16	Calcium transport	C
<i>calD</i>	Calcium	10	Calcium transport	C
<i>can</i>	Canavanine	63	Canavanine resistance	A
<i>carA</i>		1	<i>arg + ura, cap, pyrA</i> ; carbamoylphosphate synthase (EC 2.7.2.9), glutamine (light) subunit	A, C, 124, 856
<i>carB</i>		1	<i>arg + ura, cap, pyrA</i> ; carbamoylphosphate synthase (EC 2.7.2.9), ammonia (heavy) subunit	A, C, 811
<i>cbt</i>		16	Dicarboxylate-binding protein production	A, C
<i>cca</i>		67	tRNA nucleotidyl transferase (EC 2.7.7.25)	A, 231
<i>cdd</i>		46	Deoxycytidine deaminase (EC 3.5.4.5)	A, B, C, 541, 736, W
<i>cdh</i>		89	CDP-diglyceride hydrolase	C, 11, 153, 456, 499
<i>cdsA</i>		4	CDP-diglyceride synthetase (CTP:phosphatidate cytidylyltransferase) (EC 2.7.7.41)	C, 501
<i>cdsS</i>		69	Stability of CDP-diglyceride synthetase activity	358
<i>celB</i>	Celllobiose	38	Transport of celllobiose, arbutin, and salicin	595, 596, 834, J
<i>celC</i>	Celllobiose	38	Transport of celllobiose, arbutin, and salicin	595, 596, 834, J
<i>celD</i>	Celllobiose	38	Negative regulatory gene	595, 596, 834, J
<i>celF</i>	Celllobiose	38	Phospho-β-glucosidase	595, 596, 834, J
<i>cet</i>	Colicin E2	100	<i>ref, refII</i> ; tolerance to colicin E2	A, C, 287
<i>cfa</i>		36	Cyclopropane fatty acid synthase	413-415
<i>cheA</i>	Chemotaxis	42	Chemotactic response	A, B, C, 1016
<i>cheB</i>	Chemotaxis	41	Chemotactic response; protein methylesterase activity	A, B, C, 768, 1016
<i>cheR</i>	Chemotaxis	41	<i>cheX</i> ; chemotactic response; protein methylesterase activity	B, C, 768, 1016
<i>cheW</i>	Chemotaxis	42	Chemotactic response	B, 768, 1016
<i>cheY</i>	Chemotaxis	41	Chemotactic response	B, C, 201, 714, 768, 1016
<i>cheZ</i>	Chemotaxis	41	Chemotactic response	B, C, 768, 1016
<i>chlA</i>	Chlorate	18	<i>bisA, narA</i> ; biosynthesis of molybdopterin	A, B, C, 534, 901
<i>chlB</i>	Chlorate	87	<i>narB</i> ; nitrate reductase, biosynthesis of molybdopterin	A, B, C, 901
<i>chlD</i>	Chlorate	17	<i>narD</i> ; molybdenum uptake	A, B, C, 531
<i>chlE</i>	Chlorate	18	<i>bisB, narE</i> ; biosynthesis of molybdopterin	A, B, C, 534, 803, 901
<i>chlJ</i>	Chlorate	17	Molybdenum transport?	531
<i>chlM</i>	Chlorate	18	Biosynthesis of molybdopterin	534, 1084
<i>chlN</i>	Chlorate	18	Biosynthesis of molybdopterin	534, 803, 1084
<i>cirA</i>	Colicine I resistance	43	<i>feuA</i> ; production of colicin I receptor	A, B, C, 115, 408, 736, W
<i>citA</i>	Citrate	(18)	Cryptic gene of citrate transport system	429
<i>citB</i>	Citrate	(16)	Cryptic gene of citrate transport system	429
<i>cls</i>		27	Cardiolipin synthase activity	B, 817
<i>cmlA</i>	Chloramphenicol	19	Resistance or sensitivity to chloramphenicol	A, 1007
<i>coaA</i>		90	<i>panK</i> ; pantothenate kinase	1134
<i>codA</i>		8	Cytosine deaminase (EC 3.5.4.1)	A
<i>codB</i>		8	Cytosine transport	A
<i>corA</i>	Cobalt resistance	86	Mg ²⁺ transport, system I	B, C, 14
<i>corB</i>	Cobalt resistance	96	Mg ²⁺ transport, system I	B
<i>cpdB</i>		96	2',3'-Cyclic-nucleotide 2'-phosphodiesterase (EC 3.1.4.16)	C, 656
<i>cpsA</i>		44	Capsular polysaccharide synthesis	1113
<i>cpsB</i>		44	Capsular polysaccharide synthesis	1113
<i>cpsC</i>		44	Capsular polysaccharide synthesis	1113
<i>cpsD</i>		44	Capsular polysaccharide synthesis	1113
<i>cpsE</i>		44	Capsular polysaccharide synthesis	1113
<i>cpsF</i>		90	Capsular polysaccharide synthesis	1113
<i>cpxA</i>		89	F-pilus formation, surface exclusion, conjugal donor activity	C, 11-13
<i>cpxB</i>		40	F-pilus formation, surface exclusion, conjugal donor activity	C
<i>crg</i>		29	Cold-resistant growth	565
<i>crp</i>		74	<i>cap, csm</i> ; cyclic AMP receptor protein	A, C, 370, 821, 1019
<i>crr</i>		52	<i>gsr, iex, tgs</i> ; glucose phosphotransferase system enzyme III ^{Glc}	B, C, 134, 136, 270, 794, 835, 945
<i>cup</i>		98	Uptake of carbohydrates	686
<i>cxm</i>		6	<i>cxr</i> ; methylglyoxal synthesis	A, B
<i>cyaA</i>		86	Adenylate cyclase (EC 4.6.1.1)	A, B, C, 6-8, 14, 59, 70, 578, 588, 930, 931

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>cybB</i>		(16.5)	Cytochrome <i>b</i> ₅₆₁	762
<i>cycA</i>	Cycloserine	96	<i>dagA</i> ; resistance to D-cycloserine and D-serine; transport of D-alanine, D-serine, and glycine	A, B
<i>cydA</i>		17	Cytochrome <i>d</i> terminal oxidase, polypeptide subunit I	C, 400, 401
<i>cydB</i>		17	Cytochrome <i>d</i> terminal oxidase, polypeptide subunit II	A, B, 400–402
<i>cydC</i>		19	Cytochrome <i>d</i> terminal oxidase, possibly heme <i>d</i> component	371
<i>cyn</i>		8	<i>cnt</i> ; cyanate aminohydrolase (EC 3.5.5.3), cyanase	424, 1063, 1064
<i>cyo</i>		10	Cytochrome <i>o</i> terminal oxidase complex	38, 39
<i>cysA</i>	Cysteine	52	Sulfate permease; chromate resistance	A, B, 945, 1012
<i>cysB</i>	Cysteine	28	Positive regulator for <i>cys</i> regulon	A, B, 825
<i>cysC</i>	Cysteine	59	Adenosine 5'-phosphosulfate kinase (EC 2.7.1.25)	A, 640
<i>cysD</i>	Cysteine	59	ATP sulfurylase (ATP:sulfate adenyltransferase) (EC 2.7.7.4)	A, 493, 640
<i>cysE</i>	Cysteine	81	Serine acetyltransferase (EC 2.3.1.30)	A, B, 269
<i>cysG</i>	Cysteine	74	Siroheeme synthesis	A, C, 522, 679, 680
<i>cysH</i>	Cysteine	59	Adenylylsulfate reductase (EC 1.8.99.2)	A, 493, 641
<i>cysI</i>	Cysteine	59	<i>cysQ</i> ; sulfite reductase (EC 1.8.1.2), α subunit	A, 493, 641
<i>cysJ</i>	Cysteine	59	<i>cysP</i> ; sulfite reductase (EC 1.8.1.2), β subunit	A, 493, 641
<i>cysK</i>	Cysteine	52	<i>cysZ</i> ; O-Acetylserine sulfhydrylase A (EC 4.2.99.8)	B, C, 120, 134, 945, 1012
<i>cysM</i>	Cysteine	52	O-Acetylserine sulfhydrylase B (EC 4.2.99.8)	945, 1012
<i>cysN</i>	Cysteine	59	ATP-sulfurylase (ATP:sulfate adenyltransferase) (EC 2.7.7.4), subunit	640
<i>cysS</i>	Cysteine	12	Cysteinyl-tRNA synthetase (EC 6.1.1.16)	C
<i>cysT</i>	Cysteine	42	Cysteine tRNA	341, 587
<i>cytR</i>		89	Regulatory gene for <i>deo</i> operon, <i>udp</i> and <i>cdd</i>	A, B, 63, 1130
<i>dacA</i>		15	D-Alanine carboxypeptidase, fraction A; penicillin-binding protein 5	A, B, C, 141, 832, 1048
<i>dacB</i>		69	D-Alanine carboxypeptidase, fraction B; penicillin-binding protein 4	B, C
<i>dadA</i>		26	<i>dadR</i> ; D-amino acid dehydrogenase subunit	A, B, C, 1173
<i>dadB</i>		2	<i>alnA</i> ; D-amino acid dehydrogenase subunit	A, B, C
<i>dadQ</i>		99	<i>alnR</i> ; regulatory gene for <i>dad</i> regulon	A, C
<i>dadR</i>		26	Regulatory gene	1173
<i>dadX</i>		26	<i>msuA</i> ?; alanine racemase (EC 5.1.1.1)	1173
<i>dam</i>		74	DNA adenine methylase	A, B, C, 32, 139
<i>dapA</i>	Diaminopimelate	53	Dihydrodipicolinate synthase (EC 4.2.1.52)	A, 833, 909
<i>dapB</i>	Diaminopimelate	1	Dihydrodipicolinate reductase (EC 1.3.1.26)	A, C, 125
<i>dapC</i>	Diaminopimelate	4	Tetrahydrodipicolinate succinylase	A, C
<i>dapD</i>	Diaminopimelate	4	Tetrahydrodipicolinate N-succinyltransferase	A, C, 908
<i>dapE</i>	Diaminopimelate	53	<i>dapB</i> ; N-succinyl-diaminopimelate deacylase	A, 833, 909
<i>dapF</i>	Diaminopimelate	86	Diaminopimelate epimerase	907
<i>dcd</i>		(46)	<i>paxA</i> ; 2'-deoxycytidine 5'-triphosphate deaminase (EC 3.5.4.-) activity	B
<i>dcm</i>		43	<i>mec</i> ; DNA cytosine methylase	A, B, 90
<i>dcp</i>		(29)	Dipeptidyl carboxypeptidase	B
<i>dctA</i>		80	Uptake of C4-dicarboxylic acids	A
<i>dctB</i>		16	Uptake of C4-dicarboxylic acids	A
<i>ddl</i>		2	D-Alanine:D-alanine ligase	A, B, C, 914
<i>del</i>	Deletion	61	Frequency of <i>IS1</i> -mediated deletion	B
<i>deoA</i>	Deoxyribose	100	<i>tpp</i> , <i>TP</i> ; thymidine phosphorylase (EC 2.4.2.4)	A, B, C, 1127, 1128
<i>deoB</i>	Deoxyribose	100	<i>drn</i> , <i>thyR</i> ; phosphopentomutase (EC 2.7.5.6)	A, B, C, 1127
<i>deoC</i>	Deoxyribose	100	<i>dra</i> , <i>thyR</i> ; deoxyribose-phosphate aldolase (EC 4.1.2.4)	A, B, C, 243, 1126
<i>deoD</i>	Deoxyribose	100	<i>pup</i> ; purine-nucleoside phosphorylase (EC 2.4.2.1)	A, B, C, 617
<i>deoR</i>	Deoxyribose	19	<i>nucR</i> ; regulatory gene for <i>deo</i> operon	A, B, 1007, 1129
<i>dfp</i>		82	<i>dnaS</i> , <i>dut</i> ; flavoprotein affecting synthesis of DNA and pantothenate metabolism	1030, 1031
<i>dgd</i>		(70)	D-Galactose dehydrogenase production	B
<i>dgkA</i>	Diglyceride	92	Diglyceride kinase	B, C, 646
<i>dgkR</i>	Diglyceride	94	Level of diglyceride kinase	C
<i>dgoA</i>	D-Galactonate	82	2-Oxo-3-deoxygalactonate 6-phosphate aldolase (EC 4.1.2.21)	B
<i>dgoD</i>	D-Galactonate	82	Galactonate dehydratase (EC 4.2.1.6)	B
<i>dgoK</i>	D-Galactonate	82	2-Oxo-3-deoxygalactonate kinase (EC 2.7.1.58)	B
<i>dgoR</i>	D-Galactonate	82	Regulatory gene	B

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>dgoT</i>	D-Galactonate	82	Galactonate transport	B
<i>dgsA</i>		35	Function of enzyme IIA/IIB of phosphotransferase system	C, 757
<i>dicA</i>		35	Regulatory gene	80, 81
<i>dicB</i>		35	Control of cell division	80, 81
<i>dicC</i>		35	Regulatory gene	80, 81
<i>dinF</i>		92	Locus induced by UV and mitomycin C; subject to <i>recA</i> and <i>lexA</i> regulation	C, 598
<i>ddl</i>		(47)	D-Lactate dehydrogenase (EC 1.1.1.28)	C, 170, 932
<i>dms</i>		20	Dimethyl sulfoxide reductase	95
<i>dnaA</i>	DNA	83	DNA biosynthesis; initiation	A, B, C, 434, 578, 815
<i>dnaB</i>	DNA	92	<i>groP</i> , <i>grpA</i> ; DNA biosynthesis; chain elongation	A, B, C, 783
<i>dnaC</i>	DNA	99	<i>dnaD</i> ; DNA biosynthesis; initiation and chain elongation	A, B, 784, 927
<i>dnaE</i>	DNA	4	See <i>polC</i>	
<i>dnaG</i>	DNA	67	<i>dnaP</i> , <i>parB</i> ; DNA biosynthesis; primase	A, B, C, 157, 677, 765, 784, 808, 927, 1018, 1086, 1182
<i>dnaI</i>	DNA	40	DNA biosynthesis	A
<i>dnaJ</i>	DNA	0	<i>groPAB</i> , <i>groPC</i> ; DNA biosynthesis	B, 66, 814, 1196
<i>dnaK</i>	DNA	0	<i>groPAB</i> , <i>groPC</i> , <i>groPF</i> , <i>grpF</i> ; DNA biosynthesis	B, 64, 951
<i>dnaL</i>	DNA	29	<i>dnaK</i> ; DNA biosynthesis	B
<i>dnaN</i>	DNA	83	DNA biosynthesis; DNA polymerase III holoenzyme, β-subunit	C, 27, 434, 815, 894
<i>dnaQ</i>	DNA	5	<i>mutD</i> , DNA polymerase III holoenzyme, ε subunit, mutator activity	B, C, 225, 278, 298, 690, 707, 806, 971
<i>dnaT</i>	DNA	99	DNA biosynthesis; primosomal protein i	B, 709, 784
<i>dnaX</i>	DNA	11	<i>dnaZ</i> ; DNA biosynthesis; DNA polymerase III holoenzyme, τ and γ subunits; DNA elongation factor III	B, C, 335, 583, 631, 761, 927, 1207
<i>dpp</i>	Dipeptide	(14)	Transport of dipeptides	A, B
<i>drpA</i>		5	DNA and RNA biosynthesis	626
<i>dsdA</i>	D-Serine	51	D-Serine deaminase	A, B, C, 119, 724
<i>dsdC</i>	D-Serine	51	Regulatory gene for <i>dsdA</i>	A, C, 119, 723, 830
<i>dut</i>	dUTPase	82	<i>dnaS</i> , <i>sof</i> ; deoxyuridinetriphosphatase (EC 3.6.1.23)	A, B, C, 672, 673, 1031
<i>dvl</i>		7	Sensitivity to sodium dodecyl sulfate and toluidine blue plus light	1151
<i>ebgA</i>		67	Phospho-β-D-galactosidase, α subunit; cryptic gene	A, B, 430, 1050, 1051, J
<i>ebgB</i>		67	Possible homolog of <i>lacY</i> ; in <i>ebg</i> operon	430, 1051, J
<i>ebgC</i>		67	Phospho-β-D-galactosidase, β subunit; cryptic gene	430, J
<i>ebgR</i>		67	Regulatory gene	B, 430, 1051, J
<i>ecfA</i>	Energy-coupling factor	65	Pleiotropic effects on active transport coupling to metabolic energy; may be <i>metC</i>	B
<i>ecfB</i>	Energy-coupling factor	88	<i>eup</i> , <i>ssd</i> ; generalized resistance to aminoglycoside antibiotics; coupling of metabolic energy to active transport	B, C, 863
<i>eda</i>		41	<i>kdgA</i> , <i>kga</i> ; 2-keto-3-deoxygluconate 6-phosphate aldolase (EC 4.1.2.14)	A
<i>edd</i>		41	Phosphogluconate dehydratase (EC 4.2.1.12)	A
<i>endA</i>		64	DNA-specific endonuclease I	B
<i>eno</i>		60	Enolase (EC 4.2.1.11)	A, B, C, 1169
<i>entA</i>	Enterochelin	14	2,3-Dihydro-2,3-dihydroxybenzoate dehydrogenase	A, B, C, 333, 770, 850
<i>entB</i>	Enterochelin	14	2,3-Dihydro-2,3-dihydroxybenzoate synthetase	A, B, C, 333, 770, 850
<i>entC</i>	Enterochelin	14	Isochorismate synthetase	A, B, C, 333, 770, 850
<i>entD</i>	Enterochelin	13	Enterochelin synthetase, component D	A, B, C, 205, 334
<i>entE</i>	Enterochelin	14	Enterochelin synthetase, component E	A, B, C, 333, 770, 850
<i>entF</i>	Enterochelin	14	Enterochelin synthetase, component F	A, B, C, 205, 333, 845
<i>entG</i>	Enterochelin	14	Enterochelin synthetase, component G	A, B, C, 333, 770, 850
<i>envA</i>	Envelope	2	Cell envelope and cell separation	A, B, C, 71, 535, 1060
<i>envB</i>	Envelope	71	<i>mon</i> , <i>rodY</i> ; cell shape and sensitivity to antibiotics	A, B, 1147
<i>envC</i>	Envelope	81	Anomalous cell division; chain formation	A, 556
<i>envM</i>	Envelope	28	Osmotically remedial envelope defect	A
<i>envN</i>	Envelope	(4)	Osmotically remedial envelope defect	A
<i>envP</i>	Envelope	90	Osmotically remedial envelope defect	A
<i>envQ</i>	Envelope	58	Osmotically remedial envelope defect	A
<i>envT</i>	Envelope	(15)	Osmotically remedial envelope defect	A
<i>envY</i>	Envelope	13	Envelope protein; thermoregulation of porin synthesis	675

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>envZ</i>	Envelope	75	<i>ompB, perA, tpo</i> ; production of outer membrane proteins; regulatory gene	C, 179, 213, 363, 364, 748, 749, 933, 1191
<i>esp</i>		17	Site for efficient packaging of phage T1	B
<i>exbB</i>		65	Uptake of enterochelin; resistance or sensitivity to colicins	A, B, 302
<i>exbC</i>		59	Uptake of enterochelin; resistance or sensitivity to colicins	B
<i>expA</i>		22	Expression of a group of exported proteins	C
<i>exuR</i>		68	Negative regulatory gene for <i>exu</i> regulon, <i>exuT, uxuCA</i> , and <i>uxuB</i>	B, C, 489, 710
<i>exuT</i>		68	Transport of hexuronates	B, C, 102, 489, 710, 711
<i>e14</i>		26	Cryptic chromosomal element able to be excised; see <i>lit, mcrA, pin</i> and <i>sfiC</i>	137, 138, 553, 684, 861, 862, 887, 1139
<i>fabA</i>	Fatty acid biosynthesis	22	β -Hydroxydecanoyl thioester dehydrase (EC 4.2.1.60)	A, 228
<i>fabB</i>	Fatty acid biosynthesis	50	<i>fabC</i> ; β -ketoacyl-[acyl-carrier protein] synthase I (EC 2.3.1.41)	A, B, C
<i>fabD</i>	Fatty acid biosynthesis	24	Malonyl-CoA-[acyl carrier protein] transacylase (EC 2.3.1.39)	A, C
<i>fabE</i>	Fatty acid biosynthesis	71	Acetyl-CoA carboxylase (EC 6.4.1.2)	B, 1147
<i>fabF</i>	Fatty acid biosynthesis	24	<i>cvc, vtrB</i> ; β -ketoacyl-[acyl carrier protein] synthase II (EC 2.3.1.41)	B, C, 1123
<i>fadA</i>	Fatty acid degradation	87	<i>oldA</i> ; thiolase I (EC 2.3.1.16)	A, C, 1032, 1202
<i>fadB</i>	Fatty acid degradation	87	<i>oldB</i> ; 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35), 3-hydroxyacyl-CoA epimerase (EC 5.1.2.3), Δ^3 -C15- Δ^2 -trans-enoyl-CoA (EC 5.3.3.8) and enoyl-CoA-hydrolase (crotonase) (EC 4.2.1.17)	A, 1032, 1201, 1202
<i>fadD</i>	Fatty acid degradation	40	<i>oldD</i> ; acyl-CoA synthetase (EC 6.2.1.3)	A, B
<i>fadE</i>	Fatty acid degradation	5	Electron transport flavoprotein of β -oxidation	A, C
<i>fadL</i>	Fatty acid degradation	51	<i>ttr</i> ; transport of long-chain fatty acids and sensitivity to phage T2	B, 98, 99, 755
<i>fadR</i>	Fatty acid degradation	26	<i>dec, oleR, thdB</i> ; negative regulatory gene for <i>fad</i> regulon	B, C, 2, 279, F
<i>fatA</i>		69	Utilization of <i>trans</i> -unsaturated fatty acids	275
<i>fba</i>		63	<i>alc, fda</i> ; fructose-bisphosphate aldolase (EC 4.1.2.13)	A
<i>fbp</i>		96	<i>fdp</i> ; fructose-bisphosphatase (EC 3.1.3.11)	A, 578, 985
<i>fcsA</i>		86	Cell division; septation	B
<i>fdhF</i>		93	Formate dehydrogenase (formate hydrogen-lyase linked), selenopolypeptide	97, 840, 1188, 1189, 1220, 1221
<i>fdv</i>		59	<i>ant?</i> ; formate dehydrogenase-2-activity	962, 1204
<i>fecA</i>	Iron	93	Citrate-dependent iron transport, outer membrane receptor	B, C, 882, 1218
<i>fecB</i>	Iron	8	Citrate-dependent iron transport, periplasmic protein	B, C, 882, 1218
<i>fecD</i>	Iron	8	Citrate-dependent iron transport, membrane-bound protein	882
<i>feo</i>	Iron	39	Ferrous iron transport system	438
<i>fepA</i>	Iron	13	<i>cbr, cbt, feuB</i> ; receptor for ferric enterobactin (enterochelin) and colicins B and D	A, B, C, 205, 334, 676, 829, 853, 1185
<i>fepB</i>	Iron	13	Ferric enterobactin (enterochelin) uptake; periplasmic component	129, 829, 852, 853, 1185
<i>fepC</i>	Iron	13	Ferric enterobactin (enterochelin) uptake; cytoplasmic membrane component	829, 852
<i>fepD</i>	Iron	13	Ferric enterobactin (enterochelin) uptake	829
<i>fepE</i>	Iron	13	Ferric enterobactin (enterochelin) uptake	829
<i>fepF</i>	Iron	13	Ferric enterobactin (enterochelin) uptake	829
<i>fes</i>	Iron	13	Enterochelin esterase	A, B, C, 205, 334, 845
<i>fexB</i>		86	FexA phenotype affected	C
<i>ffs</i>		10	4.5S RNA	144, 486
<i>fhl</i>		58	Formate hydrogen-lyase activity, possibly electron transport system	962
<i>fhuA</i>	Ferric hydroxamate uptake	4	<i>tonA, T1, T5rec</i> ; outer membrane receptor for ferrichrome, colicin M, and phages T1, T5, and ϕ 80	129, 222, 223, 321
<i>fhuB</i>	Ferric hydroxamate uptake	4	Hydroxamate-dependent iron uptake, cytoplasmic membrane component	C, 129, 321, 591, 883
<i>fhuC</i>	Ferric hydroxamate uptake	4	Hydroxamate-dependent iron uptake, cytoplasmic membrane component	129, 154, 221, 321
<i>fhuD</i>	Ferric hydroxamate uptake	4	Hydroxamate-dependent iron uptake, cytoplasmic membrane component	129, 154, 221, 321

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>fhuE</i>	Ferric hydroxamate uptake	16	Outer membrane receptor for ferric-rhodotorulic acid	436, 968
<i>fhuF</i>	Ferric hydroxamate uptake	99	Ferric hydroxamate transport	439
<i>fic</i>		74	Filamentation in presence of cyclic AMP in mutant	1125
<i>fimA</i>	Fimbriae	98	<i>fimD</i> , <i>pilA</i> ; type 1 fimbriin (pilin), structural gene	A, B, C, 3, 304, 346, 347, 572, 575
<i>fimB</i>	Fimbriae	98	<i>pil</i> ; regulatory gene for expression of <i>himA</i>	A, B, C, 304, 573, 575
<i>fimC</i>	Fimbriae	98	<i>pil</i> ; biosynthesis of type 1 fimbriae	A, B, C, 575
<i>fimD</i>	Fimbriae	98	<i>pil</i> ; biosynthesis of type 1 fimbriae	A, B, C, 575
<i>fimE</i>	Fimbriae	98	Regulatory gene for expression of <i>fimA</i>	304, 573
<i>fimF</i>	Fimbriae	98	Fimbrial morphology	574
<i>fimG</i>	Fimbriae	98	Fimbrial morphology	574
<i>fimH</i>	Fimbriae	98	Minor fimbrial subunit, adhesin	574
<i>fipB</i>		86	Morphogenesis of phage F1	665
<i>fipC</i>		(73)	Morphogenesis of phage F1	665
<i>firA</i>		4	Affects transcription	B, 1, 210, G
<i>fis</i>		72	Site-specific DNA inversion	581
<i>fiu</i>		18	Ferric iron uptake, outer membrane protein	436
<i>flaA</i>	Flagella	24	<i>flaU</i> ; flagellar synthesis	B, C, 586
<i>flaB</i>	Flagella	24	<i>flaA</i> ; flagellar synthesis	B, C
<i>flaC</i>	Flagella	24	<i>flaW</i> ; flagellar synthesis, basal-body protein	B
<i>flaD</i>	Flagella	24	<i>flaV</i> ; flagellar synthesis, basal-body rod modification	B
<i>flaE</i>	Flagella	24	<i>flaK</i> ; flagellar synthesis, hook protein	B
<i>flaF</i>	Flagella	24	<i>flaX</i> ; flagellar synthesis, basal-body rod protein	B, C
<i>flaG</i>	Flagella	24	<i>flaL</i> ; flagellar synthesis, basal-body rod protein	B
<i>flaH</i>	Flagella	24	<i>flaY</i> ; flagellar synthesis, basal-body L-ring protein	B, C, 536
<i>flaI</i>	Flagella	24	<i>flaM</i> ; flagellar synthesis, basal-body P-ring protein	B, 536
<i>flaJ</i>	Flagella	24	<i>flaZ</i> ; flagellar synthesis	B, C
<i>flaK</i>	Flagella	24	<i>flaS</i> ; flagellar synthesis, hook-associated protein	B, C
<i>flaL</i>	Flagella	24	<i>flaT</i> ; flagellar synthesis, hook-associated protein	B
<i>fhaA</i>	Flagella	41	<i>fhaH</i> ; flagellar synthesis	A
<i>fhaB</i>	Flagella	41	<i>fhaG</i> ; flagellar synthesis	A, C
<i>fhaC</i>	Flagella	42	<i>fhaI</i> ; flagellar synthesis; regulatory gene	A, 68
<i>fhaD</i>	Flagella	42	<i>fhaB</i> ; flagellar synthesis; regulatory gene; flagellum-specific σ factor	B, C, 68
<i>fliA</i>	Flagella	43	<i>fliD</i> ; flagellar synthesis; regulation of late gene expression	A, B, C, 544, 586
<i>fliC</i>	Flagella	43	<i>fliF</i> , <i>hag</i> ; flagellin; flagellar synthesis, filament structural protein	A, B, C, 612
<i>fliD</i>	Flagella	43	<i>fliC</i> ; flagellar synthesis, hook-associated protein 2	C
<i>fliE</i>	Flagella	43	<i>fliN</i> ; flagellar synthesis	A, B, C
<i>fliF</i>	Flagella	43	<i>fliBI</i> ; flagellar synthesis, basal-body M-ring protein	A, B, C, 69
<i>fliG</i>	Flagella	43	<i>fliBII</i> ; flagellar synthesis, motor switching and energizing	A, B, C, 69
<i>fliH</i>	Flagella	43	<i>fliBIII</i> ; flagellar synthesis	A, B, C, 69
<i>fliI</i>	Flagella	43	<i>fliC</i> ; flagellar synthesis	A, B, C, 69
<i>fliJ</i>	Flagella	43	<i>fliO</i> ; flagellar synthesis	A, B, 69
<i>fliK</i>	Flagella	43	<i>fliE</i> ; flagellar synthesis, hook length control	A, B, 69
<i>fliL</i>	Flagella	43	<i>fliAI</i> ; flagellar synthesis	A, B, C, 69, 604, 696
<i>fliM</i>	Flagella	43	<i>fliAII</i> ; flagellar synthesis, motor switching and energizing	A, B, C, 202, 604
<i>fliN</i>	Flagella	43	<i>motD</i> ; flagellar synthesis, motor switching and energizing	696
<i>fliO</i>	Flagella	43	<i>fliB</i> ; flagellar synthesis	696
<i>fliP</i>	Flagella	43	<i>fliR</i> ; flagellar synthesis	A, B, C, 696
<i>fliQ</i>	Flagella	43	<i>fliQ</i> ; flagellar synthesis	A, B, 696
<i>fliR</i>	Flagella	43	<i>fliP</i> ; flagellar synthesis	A, B, 696
<i>flu</i>	Fluffing	44	Metastable gene affecting surface properties, piliation, and colonial morphology	B
<i>fnr</i>		30	<i>nirA</i> , <i>nirR</i> ; regulatory gene for nitrite and nitrate reductases, hydrogenase, and fumarate reductase	A, B, C, 994, 995
<i>folA</i>	Folate	1	<i>tmrA</i> ; dihydrofolate reductase (EC 1.5.1.3); trimethoprim resistance	A, B, C, 101
<i>folC</i>	Folate	50	Dihydrofolate:folylpolyglutamate synthetase	111, 323, 807
<i>frdA</i>		94	Fumarate reductase (EC 1.3.99.1), flavoprotein subunit	A, B, C, 538
<i>frdB</i>		94	Fumarate reductase (EC 1.3.99.1), iron-sulfur protein subunit	C, 538

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>frdC</i>		94	Fumarate reductase (EC 1.3.99.1), membrane anchor polypeptide	C, 538
<i>frdD</i>		94	Fumarate reductase (EC 1.3.99.1), membrane anchor polypeptide	C, 538
<i>frdR</i>		27	Regulation of electron transport and fermentation-associated genes; may be <i>ana</i>	546
<i>fruA</i>	Fructose	47	<i>ptsF</i> ; fructose phosphotransferase enzyme II	A, B, C, 367, W
<i>fruB</i>	Fructose	47	Fructose phosphotransferase enzyme III	367, W
<i>fruF</i>	Fructose	47	<i>fpr</i> ; phosphohistidinoprotein-hexose phosphotransferase, fructose-specific	A, B, C, 281, 367, 589, W
<i>fruK</i>	Fructose	47	<i>fpk</i> ; fructose-1-phosphate kinase (EC 2.7.1.3)	A, B, C, 115, 367, 736, W
<i>fruR</i>	Fructose	2	<i>fruC</i> ; regulatory gene; possibly repressor of <i>fru</i> operon	367, 590
<i>ftsA</i>		2	<i>divA</i> ; cell division	A, B, C, 78, 535, 913, 1059, 1206
<i>ftsE</i>		76	Cell division	B, 377, 954
<i>ftsH</i>		69	Cell division	B
<i>ftsI</i>		2	<i>pbp</i> , <i>sep</i> ; peptidoglycan synthetase; septum formation; penicillin-binding protein 3	B, C, 78, 775
<i>ftsM</i>		2	Cell division	284
<i>ftsQ</i>		76	Cell division	C, 78, 913, 914, 1206
<i>ftsS</i>		76	Cell division	377, 954
<i>ftsX</i>		76	Cell division	377
<i>ftsY</i>		76	Cell division	377
<i>ftsZ</i>		2	<i>sfb</i> , <i>sulB</i> ; cell division	B, C, 78, 535, 1059, 1205, 1206
<i>fucA</i>	Fructose	60	<i>fucC</i> ; L-fuculose-1-phosphate aldolase	A, B, 182, 190, 1013, 1217
<i>fucI</i>	Fructose	60	L-Fucose isomerase	A, B, 190, 1217
<i>fucK</i>	Fructose	60	L-Fuculose kinase (EC 2.7.1.51)	A, B, 190, 1217
<i>fucO</i>	Fructose	60	L-1,2-Propanediol oxidoreductase	A, B, 190, 1013, 1217
<i>fucP</i>	Fructose	60	Fucose permease	182, 190, 1013, 1217
<i>fucR</i>	Fructose	60	Positive regulatory protein	190, 1014, 1217
<i>fumA</i>	Fumarate	36	Regulatory gene?	421, 737, 738
<i>fumB</i>	Fumarate	93	Regulatory gene?	420, 421
<i>fumC</i>	Fumarate	36	Fumarase	420
<i>fur</i>		16	Ferric iron uptake; negative regulatory gene, repressor protein	51, 52, 266, 437, 969, K
<i>fusA</i>	Fusidic acid	73	<i>far</i> ; protein chain elongation factor EF-G	A, B, C, 1215
<i>fusB</i>	Fusidic acid	15	Pleiotropic effects on RNA synthesis, ribosomes, and ribosomal protein S6	B
<i>gabC</i>	γ-Aminobutyrate	58	Regulatory gene for <i>gabPDT</i>	A, B, C
<i>gabD</i>	γ-Aminobutyrate	58	Succinate-semialdehyde dehydrogenase (EC 1.2.1.16), NADP-dependent, activity	B, C
<i>gabP</i>	γ-Aminobutyrate	58	Transport of γ-aminobutyrate	A, B, C
<i>gabT</i>	γ-Aminobutyrate	58	Aminobutyrate aminotransferase (EC 2.6.1.19) activity	A
<i>gadR</i>		82	Regulatory gene for <i>gadS</i>	A
<i>gadS</i>		82	Glutamate decarboxylase (EC 4.1.1.15)	A
<i>galE</i>	Galactose	17	<i>galD</i> ; UDP-galactose 4-epimerase	A, B, C, 634
<i>galK</i>	Galactose	17	<i>galA</i> ; galactokinase (EC 2.7.1.6)	A, 260
<i>galP</i>	Galactose	64	<i>Pgal</i> ; galactose permease	B
<i>galR</i>	Galactose	61	<i>Rgal</i> ; regulatory gene; repressor of <i>galETK</i> operon	A, C
<i>galT</i>	Galactose	17	<i>galB</i> ; galactose-1-phosphate uridylyltransferase (EC 2.7.7.12)	A, 219, 634
<i>galU</i>	Galactose	28	Glucose-1-phosphate uridylyltransferase (EC 2.7.7.9)	A, B
<i>gap</i>		39	<i>gad</i> ; glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12)	A, B
<i>garA</i>	Glucarate	16	Glucarate utilization	C
<i>garB</i>	Glucarate	4	Glucarate utilization	C
<i>gatA</i>	Galactitol	45	Galactitol-specific enzyme II of phosphotransferase system	B, C, 655, 736
<i>gatC</i>	Galactitol	45	Regulatory gene	B, C, 655, 736
<i>gatD</i>	Galactitol	45	Galactitol-1-phosphate dehydrogenase	B, C, 655, 736
<i>gcv</i>		63	Glycine cleavage pathway	858, 1040
<i>gdhA</i>		27	Glutamate dehydrogenase	B, C, 73, 726, 1135, 1136

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>ggt</i>		76	γ-Glutamyltranspeptidase (EC 2.3.2.2)	1068, 1069
<i>gidA</i>		84	Glucose-inhibited division; chromosome replication?	152, 578, 1152
<i>gidB</i>		84	Glucose-inhibited division; chromosome replication?	578, 801, 1152
<i>glc</i>	Glycolate	65	Utilization of glycolate, malate synthase G (EC 4.1.3.2)	A
<i>glgA</i>	Glycogen	76	Glycogen synthase (EC 2.4.1.21)	A, B, C, 602
<i>glgB</i>	Glycogen	76	1,4-α-Glucan branching enzyme (EC 2.4.1.18)	A, B, C, 50
<i>glgC</i>	Glycogen	76	Glucose-1-phosphate adenylyltransferase (EC 1.7.7.27)	A, B, C, 49
<i>glk</i>		52	Glucokinase (EC 2.7.1.2)	A
<i>glmS</i>	Glucosamine	84	L-glutamine:D-fructose-6-phosphate aminotransferase (EC 2.6.1.16)	A, B, C, 1152
<i>glnA</i>	Glutamine	88	Glutamine synthetase (EC 6.3.1.2)	A, B, C, 212, 224, 742, 902, 915
<i>glnD</i>	Glutamine	4	Uridylyltransferase	B, C
<i>glnF</i>	Glutamine	70	See <i>rpoN</i>	B, C
<i>glnG</i>	Glutamine	88	<i>glnT</i> , <i>ntrC</i> ; negative regulatory gene for <i>glnA</i>	C, 682, 742
<i>glnH</i>	Glutamine	18	Periplasmic glutamine-binding protein	804, 805
<i>glnL</i>	Glutamine	88	<i>glnR</i> , <i>ntrB</i> ; negative regulatory gene for <i>glnA</i>	C, 682, 742, 805, 902, 915, 1122
<i>glnP</i>	Glutamine	18	Glutamine high-affinity transport system; membrane component	C, 805
<i>glnQ</i>		18	Glutamine high-affinity transport system	805
<i>glnR</i>	Glutamine	24	Level of glutaminyl-tRNA synthetase	C
<i>glnS</i>	Glutamine	16	Glutaminyl-tRNA synthetase (EC 6.1.1.18)	A, 864, 916, 1199
<i>glnT</i>	Glutamine	(75)	Levels of glutamine tRNA 1 and glutamine synthetase	B
<i>glnU</i>	Glutamine	15	<i>supB</i> ; glutamine tRNA 1 (tandemly duplicated gene)	B, C, 341, 587, 864
<i>glnV</i>	Glutamine	15	<i>supE</i> , <i>Su2</i> , <i>sull</i> ; glutamine tRNA 2 (tandemly duplicated gene)	B, C, 341, 587, 864
<i>glpA</i>	Glycerol phosphate	49	<i>sn</i> -Glycerol-3-phosphate dehydrogenase (anaerobic), large subunit	A, B, C, 208, 301
<i>glpB</i>	Glycerol phosphate	49	<i>sn</i> -Glycerol-3-phosphate dehydrogenase (anaerobic), membrane anchor subunit	208, 301
<i>glpC</i>	Glycerol phosphate	49	<i>sn</i> -Glycerol-3-phosphate dehydrogenase (anaerobic), small subunit	208, 301
<i>glpD</i>	Glycerol phosphate	75	<i>glyD</i> ; <i>sn</i> -glycerol-3-phosphate dehydrogenase (aerobic)	A, 980, 981
<i>glpE</i>	Glycerol phosphate	75	Gene of <i>glp</i> regulon	981
<i>glpF</i>	Glycerol phosphate	89	Facilitated diffusion of glycerol	A
<i>glpG</i>	Glycerol phosphate	75	Gene of <i>glp</i> regulon	981
<i>glpK</i>	Glycerol phosphate	89	Glycerol kinase (EC 2.7.1.30)	A, 215, 844
<i>glpQ</i>	Glycerol phosphate	49	Glycerol-3-phosphate diesterase	C, 619
<i>glpR</i>	Glycerol phosphate	75	Regulatory gene	A, 979, 981
<i>glpT</i>	Glycerol phosphate	49	<i>sn</i> -Glycerol-3-phosphate permease	A, B, C, 301, 303
<i>gltA</i>	Glutamate	16	<i>glut</i> ; citrate synthase (EC 4.1.3.7)	A, C, 110, 492, 795, 1174, 1184
<i>gltB</i>	Glutamate	70	<i>aspB</i> ; glutamate synthase, large subunit	A, B, C, 178, 360, 824
<i>gltD</i>	Glutamate	70	<i>aspB</i> ; glutamate synthase, small subunit	178, 360, 824
<i>gltE</i>	Glutamate	81	Glutamyl-tRNA synthetase; possible regulatory subunit	A
<i>gltF</i>	Glutamate	70	Regulatory gene?	178
<i>gltH</i>	Glutamate	(21)	Requirement	A
<i>gltM</i>	Glutamate	(43)	Level of glutamyl-tRNA synthetase activity	A
<i>gltR</i>	Glutamate	92	Regulatory gene for glutamate permease	A
<i>gltS</i>	Glutamate	82	<i>gltC</i> ; glutamate permease	A
<i>gltT</i>	Glutamate	90	<i>tgtB</i> ; glutamate tRNA 2; in <i>rrnB</i> operon	B, C, 587, 858, 885
<i>gltU</i>	Glutamate	85	<i>tgtC</i> ; glutamate tRNA 2; in <i>rrnC</i> operon	B, 587
<i>gltV</i>	Glutamate	90	<i>tgtE</i> ; glutamate tRNA 2; in <i>rrnE</i> operon	B, 587
<i>gltW</i>	Glutamate	56	Glutamate tRNA 2; in <i>rrnG</i> operon	C, 587
<i>gltX</i>	Glutamate	52	Catalytic subunit for glutamyl-tRNA synthetase (EC 6.1.1.17)	A, 131, 961, D
<i>glyA</i>	Glycine	55	Serine hydroxymethyltransferase (EC 2.1.2.1)	A, C, 859, 860, 1039
<i>glyS</i>	Glycine	80	<i>gly-act</i> ; glycine-tRNA synthetase (EC 6.1.1.14)	A, 132, 566
<i>glyT</i>	Glycine	90	<i>supA36</i> , <i>sumA</i> , <i>sup15B</i> ; glycine tRNA 2	A, B, C, 587
<i>glyU</i>	Glycine	62	<i>suA36</i> , <i>suD</i> , <i>sumB</i> , <i>supT</i> ; glycine tRNA 1	A, 587
<i>glyV</i>	Glycine	95	<i>suA58</i> , <i>suA78</i> ; glycine tRNA 3 (duplicate gene, tandemly triplicated)	A, B, 341, 587
<i>glyW</i>	Glycine	42	<i>suA58</i> , <i>suA78</i> ; glycine tRNA 3 (duplicate gene)	A, C, 587, 1117
<i>gnd</i>		44	Gluconate-6-phosphate dehydrogenase, (EC 1.1.1.44) decarboxylating	A, C, 788

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Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>gntR</i>	Gluconate	76	Regulatory gene for <i>edd</i> ; transport and phosphorylation of gluconate	A, B
<i>gntS</i>	Gluconate	95	<i>gntM</i> , <i>usgA</i> ; second system for transport and possibly phosphorylation of gluconate	B
<i>gntT</i>	Gluconate	75	<i>gntM</i> , <i>usgA</i> ; high-affinity transport of gluconate	A, B, 515
<i>gntV</i>	Gluconate	97	Glukokinase, thermosensitive	515
<i>gor</i>		77	Glutathione oxidoreductase (EC 1.6.4.2)	C, 308, 407
<i>gpp</i>		85	Guanosine pentaphosphatase activity	B, 14, 84
<i>gprA</i>		0	Replication of certain lambdoid phage	812
<i>gprB</i>		0	Replication of certain lambdoid phage	812
<i>gpsA</i>		81	<i>sn</i> -Glycerol-3-phosphate dehydrogenase [NAD(P) ⁺] (EC 1.1.1.94)	A, B
<i>gpt</i>		6	<i>gpp</i> , <i>gxu</i> ; guanine-hypoxanthine phosphoribosyltransferase (EC 2.4.2.8)	A, B, 523, 810, 881, 906
<i>grpD</i>		71	Initiation of phage lambda DNA replication; host DNA synthesis	B
<i>grpE</i>		57	Phage lambda replication; host DNA synthesis	B
<i>grx</i>		19	Glutaredoxin	473, 594, 934
<i>gshA</i>		58	Glutathione synthetase (EC 6.3.2.2)	B, 404, 431
<i>gsk</i>		13	Guanosine kinase	B
<i>guaA</i>	Guanine	54	<i>guaA</i> ; GMP synthetase (EC 6.3.4.1)	A, B, 1097
<i>guaB</i>	Guanine	54	<i>guaA</i> ; IMP dehydrogenase (EC 1.2.1.14)	A, B, 1089, 1090, 1094
<i>guaC</i>	Guanine	3	GMP reductase (EC 1.6.6.8)	A, F, 751, 912
<i>guaR</i>	Guanine	54	Regulatory gene	1096
<i>gurB</i>		74	Utilization of methyl-β-D-glucuronide; possibly <i>crp</i>	A
<i>gurC</i>		(18)	Utilization of methyl-β-D-glucuronide	A
<i>gurD</i>		(68)	Utilization of methyl-β-D-glucuronide	A
<i>gyrA</i>	Gyrase	48	<i>nalA</i> ; DNA gyrase (EC 5.99.1.3), subunit A; resistance or sensitivity to nalidixic acid	A, B, C, 497, 732, 733, 1208
<i>gyrB</i>	Gyrase	83	<i>acrB</i> , <i>cou</i> , <i>himB</i> , <i>nalC</i> , <i>pcbA</i> ; DNA gyrase (EC 5.99.1.3), subunit B; resistance or sensitivity to coumermycin	B, C, 4, 5, 732, 733, 1197
<i>hemA</i>	Hemin	27	Glutamyl-tRNA dehydrogenase	A, 42
<i>hemB</i>	Hemin	8	<i>ncf</i> ; 5-aminolevulinate dehydratase (EC 4.2.1.24) activity	A, B, 642
<i>hemC</i>	Hemin	86	<i>popE</i> ; porphobilinogen deaminase (EC 4.3.1.18)	B, 539, 965, 966, 1091
<i>hemD</i>	Hemin	86	Uroporphyrinogen III synthase (EC 4.2.1.75)	B, 539, 540, 965, 966
<i>hemE</i>	Hemin	90	<i>hemC</i> ; uroporphyrinogen decarboxylase (EC 4.1.1.37)	A
<i>hemF</i>	Hemin	17	<i>popB</i> , <i>sec</i> ; coproporphyrinogen III oxidase (EC 1.3.3.3)	A
<i>hemG</i>	Hemin	87	Protoporphyrinogen oxidase activity	C
<i>hemH</i>	Hemin	11	<i>hemG</i> , <i>popA</i> ; ferrochelatase (EC 4.99.1.1)	A
<i>het</i>		84	<i>cop</i> ; binding of DNA sequences in <i>oriC</i> region to outer membrane; possibly structural gene for DNA-binding protein	A, C
<i>herC</i>		62	Suppressor of ColE1 mutation in primer RNA	564
<i>hflB</i>		69	Lysogeny and level of phage lambda cII protein	62
<i>hflC</i>		95	<i>hflA</i> ; high frequency of lysogenization by phage lambda	61
<i>hflK</i>		95	<i>hflA</i> ; high frequency of lysogenization by phage lambda	61
<i>himA</i>		37	<i>hid</i> ; integration host factor (IHF), α subunit; site-specific recombination	C, 727, 728
<i>himD</i>		20	<i>hip</i> ; integration host factor (IHF), β subunit; site-specific recombination	C, 332, 567
<i>hipA</i>		34	Frequency of persistence following inhibition of murein synthesis	759, 760
<i>hisA</i>	Histidine	44	<i>N</i> -(5'-phospho-L-ribosylformimino)-5-amino-1-(5'-phosphoribosyl)-4-imidazolecarboxamide isomerase (EC 5.3.1.16)	A
<i>hisB</i>	Histidine	44	Imidazoleglycerolphosphate dehydratase (EC 4.2.1.19) and histidinol phosphate phosphatase (EC 3.1.3.15)	A, 193, 410
<i>hisC</i>	Histidine	44	Histidinol phosphate aminotransferase (EC 2.6.1.9)	A, 409, 410
<i>hisD</i>	Histidine	44	L-Histidinol:NAD ⁺ oxidoreductase (EC 1.1.1.23)	A, C, 192
<i>hisE</i>	Histidine	44	See <i>hisI</i>	A
<i>hisF</i>	Histidine	44	Cyclase	A
<i>hisG</i>	Histidine	44	ATP phosphoribosyltransferase (EC 2.4.2.17)	A, B, C
<i>hisH</i>	Histidine	44	Amido transferase	A
<i>hisI</i>	Histidine	44	<i>hisE</i> ; phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19), phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31)	A, 192

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>hisJ</i>	Histidine	50	Histidine-binding protein of high-affinity histidine transport system	C
<i>hisM</i>	Histidine	50	Histidine transport	592
<i>hisP</i>	Histidine	50	Histidine permease	C, 592
<i>hisR</i>	Histidine	(86)	<i>hisT</i> ; histidine tRNA	B, 485, 587
<i>hisS</i>	Histidine	54	Histidinyl-tRNA synthetase (EC 6.1.1.21)	B, C, 345
<i>hisT</i>	Histidine	50	<i>asuC</i> , <i>leuK</i> ; pseudouridylate synthase I	B, C, 29–31, 708, 807, 984
<i>hlpA</i>		4	<i>skp</i> ; histonelike protein HLP-I (BH1); DNA-binding nucleoid-associated protein	1, 210, 469, 621, G
<i>hns</i>		6	Histonelike protein HLP-II (HU, BH2, HD, NS); DNA-binding protein	870
<i>hpt</i>		3	Hypoxanthine phosphoribosyltransferase	A
<i>hsdM</i>	Host specificity	99	<i>hs</i> , <i>hsm</i> , <i>hsp</i> , <i>rm</i> ; host modification; DNA methylase M	A, C, 660
<i>hsdR</i>	Host specificity	99	<i>hs</i> , <i>hsp</i> , <i>hsr</i> , <i>rm</i> ; host restriction; endonuclease R	A, C, 660
<i>hsdS</i>	Host specificity	99	<i>hss</i> ; specificity determinant for <i>hsdM</i> and <i>hsdR</i>	A, C, 391, 660, 767
<i>htpG</i>		11	Heat shock protein C 62.5	65
<i>htpR</i>			See <i>rpoH</i>	
<i>hupB</i>		10	Histonelike protein HU-1 (HU-β, NS1)	551, 552, 1053
<i>hydA</i>		58	Hydrogenase 1 activity	557, 629, 962
<i>hydB</i>		59	Hydrogenase activity	629, 962, 1161
<i>hydC</i>		77	Formate hydrogenlyase activity and fumarate-dependent H ₂ uptake; possibly nickel metabolism	1187
<i>hydD</i>		77	Formate hydrogen-lyase activity and fumarate-dependent H ₂ uptake	1187
<i>hydE</i>		59	Hydrogenase activity	188
<i>hydL</i>		65	<i>hup</i> ?; hydrogenase L, possibly same as hydrogenase 3; hydrogen uptake	629, 1047
<i>iap</i>		59	Alkaline phosphatase isozyme conversion	B, 512, 780
<i>icd</i>		26	Isocitrate dehydrogenase, NADP ⁺ specific (EC 1.1.1.42)	B, C
<i>iclR</i>		91	Regulatory gene for <i>aceBA</i> operon	A, C
<i>ileR</i>		100	<i>avr</i> , <i>ftrA</i> ?; negative regulatory gene of <i>thr</i> and <i>ilv</i> operons	532, 533, 1164
<i>ileS</i>	Isoleucine	0	Isoleucyl-tRNA synthetase (EC 1.1.1.5)	A, B, 549, 741, 899, 1102, 1192, 1196
<i>ileT</i>	Isoleucine	87	<i>tilA</i> ; isoleucine tRNA 1; in <i>rrnA</i> operon	B, 587
<i>ileU</i>	Isoleucine	72	<i>tilD</i> ; isoleucine tRNA 1; in <i>rrnD</i> operon	B, 587
<i>ileV</i>	Isoleucine	5	Isoleucine tRNA 1; in <i>rrnH</i> operon	C, 587
<i>ileX</i>	Isoleucine	67	Isoleucine tRNA 2	766
<i>ilvA</i>	Isoleucine-valine	85	<i>ile</i> ; threonine deaminase (EC 4.2.1.16)	A, B, C, 14, 285, 623
<i>ilvB</i>	Isoleucine-valine	83	Acetohydroxy acid synthase I (EC 4.1.3.18), valine-sensitive, large subunit	A, B, C, 349, 350, 448, 543, 993, 1167
<i>ilvC</i>	Isoleucine-valine	85	<i>ilvA</i> ; ketol-acid reductoisomerase (EC 1.1.1.86)	A, B, C, 14, 70, 1165
<i>ilvD</i>	Isoleucine-valine	85	<i>ilvB</i> ; dihydroxyacid dehydratase (EC 4.2.1.9)	A, B, C, 14, 285, 623
<i>ilvE</i>	Isoleucine-valine	85	<i>ilvC</i> , <i>ilvJ</i> ; branched-chain amino-acid aminotransferase (EC 2.6.1.42)	A, B, C, 14, 168, 285, 606, 623, 664, 1166
<i>ilvF</i>	Isoleucine-valine	54	Acetohydroxy acid synthase (valine insensitive) activity	A
<i>ilvG</i>	Isoleucine-valine	85	Acetohydroxy acid synthase II (EC 4.1.3.18), valine-insensitive, large subunit	A, B, C, 14, 285, 623, 670
<i>ilvH</i>	Isoleucine-valine	2	Acetohydroxy acid synthase III (EC 4.1.3.18), valine-sensitive, small subunit	A, B, C, 1037
<i>ilvI</i>	Isoleucine-valine	2	Acetohydroxy acid synthase III (EC 4.1.3.18), valine-sensitive, large subunit	A, B, C, 447, 1037
<i>ilvJ</i>	Isoleucine-valine	2	Acetohydroxy acid synthase IV (EC 4.1.3.18), valine-insensitive	C
<i>ilvM</i>	Isoleucine-valine	85	Acetohydroxy acid synthase II (EC 4.1.3.18), valine-insensitive, small subunit	623, 664, 670, 1166
<i>ilvN</i>	Isoleucine-valine	83	Acetohydroxy acid synthase II (EC 4.1.3.18), valine-sensitive, small subunit	349, 1167
<i>ilvR</i>	Isoleucine-valine	100	Positive regulatory gene of <i>thr</i> and <i>ilv</i> operons	533
<i>ilvU</i>	Isoleucine-valine	7	Regulation of <i>ileS</i> and modification of isoleucine tRNA 2 and valine tRNA 2	C
<i>ilvY</i>	Isoleucine-valine	85	Positive regulatory locus for <i>ilvC</i>	B, C, 14, 1165
<i>infA</i>		20	Protein chain initiation factor 1	960
<i>infB</i>		69	<i>ssyG</i> ; protein chain initiation factor 2	C, 510, 776, 865, 866, 868, 999–1001

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>infC</i>		38	<i>fit?</i> ; protein chain initiation factor 3	B, C, 158, 249, 306, 717, 878, 1170, 1190
<i>inm</i>		(79)	Susceptibility to mutagenesis by nitrosoguanidine	C
<i>ior</i>		45	Radiation sensitivity, particularly γ rays; recombination ability decreased	317
<i>katC</i>	Catalase	7	Catalase activity	B
<i>katE</i>	Catalase	38	Biosynthesis of catalase hydroperoxidase HPII (III)	661, 662
<i>katF</i>	Catalase	59	<i>nur</i> ; biosynthesis of catalase hydroperoxidase HPII (III) and exonuclease III; regulatory gene	662, 950, 955
<i>katG</i>	Catalase	89	Catalase-peroxidase hydroperoxidase HPI (I), structural gene	663, 1112
<i>kba</i>		69	Ketose-bis-phosphate aldolase, temperature-sensitive enzyme, active on D-tagatose-1,6-diphosphate	B
<i>kbl</i>		81	2-Amino-3-ketobutyrate CoA ligase (EC 2.3.1.29) (glycine acetyltransferase)	28, 892
<i>kdgK</i>	Ketodeoxygluconate	78	Ketodeoxygluconokinase (EC 2.7.1.45)	A
<i>kdgR</i>	Ketodeoxygluconate	40	Regulatory gene for <i>kdgK</i> , <i>kdgT</i> , and <i>eda</i>	A
<i>kdgT</i>	Ketodeoxygluconate	88	2-Keto-3-deoxy-D-gluconate transport system	A, B, 698
<i>kdpA</i>	Potassium dependence	16	<i>kac</i> ; high-affinity potassium transport system; probably K ⁺ -stimulated ATPase	A, B
<i>kdpB</i>	Potassium dependence	16	<i>kac</i> ; high-affinity potassium transport system	A, B
<i>kdpC</i>	Potassium dependence	16	<i>kac</i> ; high-affinity potassium transport system	A, B
<i>kdpD</i>	Potassium dependence	16	<i>kac</i> ; high-affinity potassium transport system; regulatory gene	A, B
<i>kdsA</i>		27	3-Deoxy-D-manno-octulosonic acid 8-phosphate synthase	1180, 1181
<i>kdsB</i>		85	CTP: CMP-3-deoxy-D-manno-octulosonate cytidyltransferase	382, 383, 848
<i>kefB</i>	K ⁺ efflux	73	<i>trkB</i> ; NEM-activatable K ⁺ /H ⁺ antiporter	A, 54
<i>kefC</i>	K ⁺ efflux	1	<i>trkC</i> ; NEM-activatable K ⁺ /H ⁺ antiporter	54
<i>ksgA</i>	Kasugamycin	1	S-Adenosylmethionine-6-N',N'-adenosyl (tRNA) dimethyltransferase	A, C, 101, 1138
<i>ksgB</i>	Kasugamycin	37	Second step (high-level) resistance to kasugamycin	A, B, C, 415
<i>ksgC</i>	Kasugamycin	12	Kasugamycin resistance; affects ribosomal protein S2	B
<i>ksgD</i>	Kasugamycin	31	Kasugamycin resistance	C
<i>lacA</i>	Lactose	8	<i>a</i> , <i>lacAc</i> ; galactoside acetyltransferase (EC 2.3.1.18)	A, B, 453
<i>lacI</i>	Lactose	8	<i>i</i> ; regulatory gene; repressor protein of <i>lac</i> operon	A, B, C, 478
<i>lacY</i>	Lactose	8	<i>y</i> ; galactoside permease (M protein)	A, B, C
<i>lacZ</i>	Lactose	8	<i>z</i> ; β -D-galactosidase (EC 3.2.1.23)	A, B, C, 547
<i>lamB</i>	Lambda	92	<i>malB</i> ; phage lambda receptor protein; maltose high-affinity uptake system	A, B, C
<i>lct</i>	Lactate	81	D-Lactate dehydrogenase (EC 1.1.1.27)	A, 653
<i>lepA</i>		55	GTP-binding membrane protein; function unknown	700, 701
<i>lepB</i>		55	Leader peptidase (signal peptidase I)	C, 700, 1183
<i>leuA</i>	Leucine	2	α -Isopropylmalate synthase (EC 4.1.3.12)	A, C, 368
<i>leuB</i>	Leucine	2	β -Isopropylmalate dehydrogenase (EC 1.1.1.85)	A, C
<i>leuC</i>	Leucine	2	α -Isopropylmalate isomerase subunit	A, C
<i>leuD</i>	Leucine	2	α -Isopropylmalate isomerase subunit	A, C
<i>leuJ</i>	Leucine	14	<i>ftr</i> ; regulation of <i>leu</i> and <i>ilv</i> operons	532
<i>leuK</i>	Leucine	19	See <i>hisT</i>	
<i>leuR</i>	Leucine	79	Level of leucyl-tRNA synthetase	B
<i>leuS</i>	Leucine	15	Leucyl-tRNA synthetase (EC 6.1.1.4)	A, B, C, 444
<i>leuT</i>	Leucine	(86)	Leucine tRNA 1 (duplicate gene)	B, 485, 587
<i>leuU</i>	Leucine	(69)	Leucine tRNA 2	B, 587, 1150
<i>leuV</i>	Leucine	(99)	Leucine tRNA 1 (duplicate gene, tandemly triplicated)	B, 289, 341, 587
<i>leuW</i>	Leucine	15	Leucine tRNA 3	B, C, 587, 864
<i>leuX</i>	Leucine	97	<i>Su-6</i> , <i>supP</i> ; leucine tRNA 5	B, C, 587, 1092, 1210
<i>leuY</i>	Leucine	10	Level of leucyl-tRNA synthetase	B
<i>leuZ</i>	Leucine	42	Leucine tRNA 4	587
<i>lev</i>	Levallorphan	(9)	Resistance to levallorphan	B
<i>lexA</i>		92	<i>exrA</i> , <i>spr</i> , <i>tsl</i> , <i>umuA</i> ; regulatory gene for SOS operon	A, B, C
<i>lig</i>	Ligase	52	<i>dnaL</i> , <i>pdeC</i> ; DNA ligase	A, B, 513
<i>linB</i>	Lincomycin	(29)	High-level resistance to lincomycin	A
<i>lip</i>	Lipoate	15	Requirement	A, C
<i>lit</i>		25	Phage T4 late-gene expression; locus of element e14	B, 553, 554, L
<i>livG</i>	Leucine, isoleucine, and valine	76	High-affinity branched-chain amino acid transport system; membrane component	C, 791

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>livH</i>	Leucine, isoleucine, and valine	76	High-affinity branched-chain amino acid transport system; membrane component	B, C, 790
<i>livJ</i>	Leucine, isoleucine, and valine	76	High-affinity branched-chain amino acid transport system; periplasmic binding protein for leucine, isoleucine, and valine	B, C, 613, 1098
<i>livK</i>	Leucine, isoleucine, and valine	76	High-affinity branched-chain amino acid transport system	B, C, 613, 790, 791, 1098
<i>livL</i>	Leucine, isoleucine, and valine	76	leucine-specific periplasmic binding protein	P
<i>livM</i>	Leucine, isoleucine, and valine	76	High-affinity branched-chain amino acid transport	790, 791
<i>livR</i>	Leucine, isoleucine, and valine	20	<i>lss</i> , <i>lstR</i> ; high-affinity branched-chain amino acid transport system; regulatory gene; repressor protein	B, 25, P
<i>lon</i>	Long form	10	<i>capR</i> , <i>deg</i> , <i>dir</i> , <i>muc</i> ; DBA-binding, ATP-dependent protease La	A, B, C, 366
<i>lpcA</i>	Lipopolysaccharide core	6	<i>tfrA</i> ; lipopolysaccharide core synthesis; resistance to phages T4, T7, and P1; deficiency in conjugation	A, B, Q
<i>lpcB</i>	Lipopolysaccharide core	(65)	<i>pon</i> ; lipopolysaccharide core synthesis	A
<i>lpd</i>		3	<i>dhl</i> ; lipoamide dehydrogenase (NADH) (EC 1.6.4.3)	A, B, C, 422, 1029, 1044
<i>lpp</i>	Lipoprotein	36	<i>mlpA</i> ; murein lipoprotein structural gene	B, C, 415
<i>lpxA</i>		4	UDP-N-acetylglucosamine acetyltransferase	210, 229, 230
<i>lpxB</i>		4	<i>pgsB</i> ; lipid A disaccharide synthase	210, 229, 230, 1103
<i>lrs</i>		3	Level of leucine tRNA	C
<i>lspA</i>		1	Prolipoprotein signal peptidase (SPaseII)	B, 505, 549, 741, 899, 1102, 1192, 1195, 1196, 1212
<i>lysA</i>	Lysine	61	Diaminopimelate decarboxylase (EC 4.1.1.20)	A, C, 1054, 1056
<i>lysC</i>	Lysine	91	<i>apk</i> ; aspartokinase III	A, B, C, 175, 176
<i>lysR</i>	Lysine	61	Positive regulatory gene	1055, 1056
<i>lysS</i>	Lysine	62	Lysyl tRNA synthetase, constitutive	186, 310
<i>lysT</i>	Lysine	17	<i>suβ</i> , <i>supG</i> , <i>supL</i> ; lysine tRNA (duplicated gene)	B, 341, 587, 880, 1211
<i>lysU</i>	Lysine	94	Lysyl tRNA synthetase, inducible	186, 1137
<i>lysV</i>	Lysine	52	<i>supN</i> ; lysine tRNA (duplicated gene)	A, 587, 1121, D
<i>lysX</i>	Lysine	60	Lysine excretion	A
<i>lytA</i>		58	Tolerance to β-lactams; autolysis defective?	442, 1004
<i>mac</i>	Macrolide	(27)	Erythromycin growth dependence	A
<i>mafA</i>		1	Maintenance of F-like plasmids	A, B
<i>mafB</i>		2	Maintenance of F-like plasmids	B
<i>malE</i>	Maltose	92	<i>malB</i> ; periplasmic maltose-binding protein; substrate recognition for transport and chemotaxis	A, B, C, 75, 76, 294, 816
<i>malF</i>	Maltose	92	<i>malB</i> ; maltose transport; cytoplasmic membrane protein	A, B, 353
<i>malG</i>	Maltose	92	<i>malB</i> ; active transport of maltose and maltodextrins	B, 251, 344
<i>mall</i>	Maltose	36	Production of oligosaccharide, probably glucose polymer	300
<i>malK</i>	Maltose	92	<i>malB</i> ; maltose permeation	A, B, C, 75, 76, 379, 816
<i>mallM</i>	Maltose	92	<i>molA</i> ; periplasmic protein; function not known	380
<i>malP</i>	Maltose	75	<i>malA</i> ; maltodextrin phosphorylase (EC 2.4.1.1)	A, B, C
<i>malQ</i>	Maltose	75	<i>malA</i> ; amylosemaltase (EC 2.4.1.25)	A
<i>malS</i>	Maltose	80	α-Amylase	348
<i>malT</i>	Maltose	75	<i>malA</i> ; positive regulatory gene for <i>mal</i> regulon	A, B, C, 209
<i>manA</i>	Mannose	36	<i>pmi</i> ; mannose-6-phosphate isomerase (EC 5.3.1.8)	A, C, 737, 738
<i>manC</i>	Mannose	(88)	<i>mini</i> ; D-mannose isomerase regulation; utilization of D-lyxose	B
<i>manX</i>	Mannose	40	<i>gptB</i> , <i>mpt</i> , <i>ptsL</i> , <i>ptsM</i> , <i>ptsX</i> ; mannose phosphotransferase system, protein II-A (III)	313, 315, 831, 1175
<i>manY</i>	Mannose	40	<i>pel</i> , <i>ptsP</i> , <i>ptsM</i> ; mannose phosphotransferase system; Pel protein II-P; penetration of phage lambda	313, 315, 831, 1175
<i>manZ</i>	Mannose	40	<i>gptB</i> , <i>mpt</i> , <i>ptsM</i> , <i>ptsX</i> ; mannose phosphotransferase system, enzyme IIB (II M)	831, 1175
<i>mara</i>		34	Multiple antibiotic resistance; tetracycline efflux system	369
<i>mcra</i>		25	<i>rglA</i> ; restriction of DNA at 5-methyl cytosine residues; locus of e14	887, 888, 890, L
<i>mcrB</i>		98	<i>rglB</i> ; restriction of DNA at 5-methylcytosine residues	887, 888, 890, 924, 925
<i>mdh</i>		70	Malate-dehydrogenase (EC 1.1.1.37)	A, 718, 1067, 1144
<i>mdoA</i>	Membrane-derived oligosaccharides	23	Membrane-localized component of glucosyl transferase system	112

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>mdoB</i>	Membrane-derived oligosaccharides	99	Phosphoglycerol transferase I activity	325, 521
<i>melA</i>	Melibiose	93	<i>mel-7</i> ; α -galactosidase (EC 3.2.1.22)	A, 433, 648, 1003, 1162
<i>melB</i>	Melibiose	93	<i>mel-4</i> ; thiomethylgalactoside permease II	A, 433, 1203
<i>melR</i>	Melibiose	93	Regulatory gene	1162
<i>menA</i>	Menaquinone	89	Conversion of 1,4-dihydroxy-2-naphthoate to demethyl-menaquinone	A, B
<i>menB</i>	Menaquinone	49	1,4-Dihydroxy-2-naphthoate synthase	B, C, 996, 997
<i>menC</i>	Menaquinone	49	Conversion of chorismate to α -succinylbenzoate	B, C, 996, 997
<i>menD</i>	Menaquinone	49	Menaquinone biosynthesis	C, 996, 997
<i>menE</i>	Menaquinone	49	α -Succinylbenzoate-CoA synthase	996
<i>mepA</i>		50	Murein DD-endopeptidase	503
<i>metA</i>	Methionine	91	<i>met₃</i> ; homoserine transsuccinylase (EC 2.3.1.46)	A, C, 734, N
<i>metB</i>	Methionine	89	<i>met₁</i> , <i>met₂</i> ; cystathione γ -synthase (EC 4.2.99.9)	A, C, 288, 405, 406, 569, 647, 946
<i>metC</i>	Methionine	65	Cystathione γ -lyase (EC 4.4.1.1)	A, 82, 735
<i>metD</i>	Methionine	5	High-affinity uptake of D- and L-methionine	A, B
<i>metE</i>	Methionine	86	<i>metB₁₂</i> ; tetrahydropteroylglutamate methyltransferase (EC 2.1.1.14)	A, 14, 15, 822
<i>metF</i>	Methionine	89	<i>met₂</i> , <i>met₃</i> ; 5,10-methylenetetrahydrofolate reductase (EC 1.1.1.68)	A, C, 405, 569, 946, 947, 1111
<i>metG</i>	Methionine	(46)	Methionyl-tRNA synthetase	A, B, 245
<i>metH</i>	Methionine	91	B ₁₂ -dependent homocysteine-N ⁵ -methyltetrahydrofolate transmethylase	A, B, 822, N
<i>metJ</i>	Methionine	89	Regulatory gene; repressor of <i>metF</i>	A, B, C, 405, 569, 647, 946, 1020
<i>metK</i>	Methionine	64	Methionine adenosyltransferase (EC 2.5.1.6)	A, B, 127, 705
<i>metL</i>	Methionine	89	<i>metM</i> ; aspartokinase II (EC 2.7.2.4), homoserine dehydrogenase II (EC 1.1.1.3)	A, C, 288, 405, 406, 569, 946, 1214
<i>metR</i>	Methionine	86	Regulatory gene for <i>metE</i> and <i>metH</i>	1124
<i>metT</i>	Methionine	15	Methionine tRNA _m (duplicated gene)	B, C, 341, 587, 864
<i>metY</i>	Methionine	(69)	Methionine tRNA _{f2} (tandemly duplicated gene)	B, 510, 511, 587
<i>metZ</i>	Methionine	(60)	Methionine tRNA _{f1} (tandemly duplicated gene)	B, 587, 769
<i>mglA</i>	Methyl-galactoside	46	<i>mglP</i> ; methyl-galactoside transport and galactose taxis, cytoplasmic membrane protein	A, B, C, 115, 440, 736, 975, W
<i>mglB</i>	Methyl-galactoside	46	<i>mglP</i> ; galactose-binding protein; receptor for galactose taxis	A, B, C, 440, 736, 975, 982, W
<i>mglC</i>	Methyl-galactoside	46	<i>mglP</i> ; methyl-galactoside transport and galactose taxis	A, B, C, 440, 736, W
<i>mglD</i>	Methyl-galactoside	45	Regulatory locus for methyl-galactoside transport	B, C
<i>mglR</i>	Methyl-galactoside	(16)	R-MG; regulatory gene	A
<i>mgt</i>		93	Mg ²⁺ transport, system II	B
<i>miaA</i>	Magnesium transport	95	<i>trpX</i> ; 2-methylthio-N ⁶ -isopentyladenosine hypermodification	357
<i>micF</i>		48	<i>stc</i> ; regulatory antisense RNA affecting <i>ompF</i> expression	20, 743, 747, 756
<i>minB</i>	Minicell	26	Formation of minute cells containing no DNA; complex locus; position of division septum	A, C, 259
<i>mioC</i>		84	Initiation of chromosome replication	659
<i>mmrA</i>		85	Recovery in rich medium following UV irradiation	990
<i>mng</i>	Manganese	(39)	Resistance or sensitivity to manganese	A
<i>mopA</i>	Morphogenesis of phages	94	<i>groE</i> , <i>groEL</i> , <i>hdh</i> , <i>tabB</i> ; head assembly of phages T4 and lambda	A, B, C
<i>mopB</i>	Morphogenesis of phages	94	<i>groE</i> , <i>groES</i> , <i>hdh</i> , <i>tabB</i> ; head assembly of phages T4 and lambda	A, B, C
<i>motA</i>	Motility	42	<i>flaJ</i> ; flagellar paralysis	A, B, 258, 1016
<i>motB</i>	Motility	42	<i>flaJ</i> ; flagellar paralysis	A, B, 1016, 1038
<i>mraA</i>	Murein	2	D-Alanine carboxypeptidase	A
<i>mraB</i>	Murein	2	D-Alanine requirement; cell wall peptidoglycan biosynthesis	A
<i>mrbA</i>	Murein	90	UDP-N-acetylglucosaminyl-3-enolpyruvate reductase activity	A
<i>mrbB</i>	Murein	90	D-Alanine requirement; cell wall peptidylglycan biosynthesis	A
<i>mrbC</i>	Murein	90	Cell wall peptidylglycan biosynthesis	A
<i>mrcA</i>	Murein	75	<i>ponA</i> ; peptidoglycan synthetase; cell wall synthesis; penicillin-binding protein 1A	B, C, 140

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>mrcB</i>	Murein	75	<i>ponB</i> ; peptidoglycan synthetase; cell wall synthesis; penicillin-binding protein 1Bs	B, C, 140, 562, 917
<i>mrdA</i>		15	<i>pbpA</i> ; cell shape; penicillin-binding protein 2	B, C, 35, 36, 78, 1048, 1049
<i>mrdB</i>		15	<i>rodA</i> ; cell shape; sensitivity to radiation and drugs	A, B, C, 35, 36, 78, 1048, 1049
<i>mre</i>		71	Cell shape; sensitivity to antibiotics	1147
<i>mrr</i>		99	Restriction of methylated adenine	454
<i>mtlA</i>	Mannitol	81	Mannitol-specific enzyme II of phosphotransferase system	A, B, C, 628
<i>mtlC</i>	Mannitol	81	Regulatory locus	A, B
<i>mtlD</i>	Mannitol	81	Mannitol-1-phosphate dehydrogenase (EC 1.1.1.17)	A, B, C
<i>mtr</i>	Methyltryptophan	69	Resistance to 5-methyltryptophan	A, B
<i>mul</i>		83	Mutability of UV-irradiated phage λ	A
<i>murC</i>	Murein	2	L-Alanine-adding enzyme	A, B, C
<i>murE</i>	Murein	2	<i>meso</i> -Diaminopimelate-adding enzyme	A, B
<i>murF</i>	Murein	2	<i>mra</i> ; D-alanyl:D-alanine-adding enzyme	A, B
<i>murG</i>	Murein	2	Murein or envelope biosynthesis	C
<i>murH</i>	Murein	99	Peptidoglycan synthesis, late stage	238
<i>mutD</i>	Mutator	5	See <i>dnaQ</i>	
<i>mutH</i>	Mutator	61	<i>mutR</i> , <i>prv</i> ; methyl-directed mismatch repair	A, B, 398, 399
<i>mutL</i>	Mutator	95	<i>mut-25</i> ; methyl-directed mismatch repair	A
<i>mutM</i>	Mutator	82	G · C → T · A transversions	165
<i>mutS</i>	Mutator	59	Methyl-directed mismatch repair	A, B
<i>mutT</i>	Mutator	2	A · T → C · G transversions; a nucleoside triphosphate	A, B, 9, 91
<i>mutY</i>	Mutator	64	G · C → T · A transversions	800
<i>mvrA</i>		7	Resistance or sensitivity to methyl viologen	753
<i>nadA</i>	NAD	17	<i>nicA</i> ; quinolinate synthetase, A protein	A
<i>nadB</i>	NAD	56	<i>nicB</i> ; quinolinate synthetase, B protein	A
<i>nadC</i>	NAD	3	Quinolinate phosphoribosyl transferase	A, C, 422, 912
<i>nagA</i>	<i>N</i> -Acetylglucosamine	16	<i>N</i> -Acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)	A, 864
<i>nagB</i>	<i>N</i> -Acetylglucosamine	16	<i>glmD</i> ; glucosamine-6-phosphate deaminase	A, 864, 916
<i>nagE</i>	<i>N</i> -Acetylglucosamine	16	<i>ptsN</i> ; <i>N</i> -acetylglucosamine-specific enzyme II of phosphotransferase system	C, 864, 916
<i>nalA</i>	Nalidixic acid	48	See <i>gyrA</i>	
<i>nalB</i>	Nalidixic acid	58	Resistance or sensitivity to nalidixic acid	A
<i>nalD</i>	Nalidixic acid	89	Penetration of nalidixic acid through outer membrane	484
<i>nanA</i>		70	<i>N</i> -Acetylneuraminate lyase (aldolase) (EC 4.1.3.3)	1143
<i>nanT</i>		70	Sialic acid transport	1143
<i>narG</i>	Nitrate reductase	27	<i>chlC</i> , <i>narC</i> ; nitrate reductase (EC 1.7.99.4), α subunit	A, B, C, 299, 427, 643, 644, 725, 920, 1024
<i>narH</i>	Nitrate reductase	27	<i>chlC</i> ; nitrate reductase (EC 1.7.99.4), β subunit	A, B, C, 299, 1024
<i>narI</i>	Nitrate reductase	27	<i>chlI</i> ; cytochrome <i>b</i> _{NR} , nitrate reductase (EC 1.7.99.4), γ subunit	A, B, C, 427, 920, 1024
<i>narJ</i>	Nitrate reductase	27	Nitrate reductase (EC 1.7.99.4), δ subunit	1024
<i>narK</i>	Nitrate reductase	27	Regulatory gene	1046
<i>narL</i>	Nitrate reductase	27	<i>narR</i> ; regulatory gene	518, 1046
<i>narX</i>	Nitrate reductase	27	<i>narR</i> ; regulatory gene	1046
<i>narZ</i>	Nitrate reductase	33	Cryptic gene(s) encoding a second nitrate reductase	114
<i>ndh</i>		22	Respiratory NADH dehydrogenase	B, C
<i>neaB</i>	Neamine	74	Resistance to neamine	A, B
<i>nek</i>		73	<i>amk</i> ; resistance to neomycin, kanamycin, and other aminoglycoside antibiotics	A, B
<i>nfnA</i>		80	Sensitivity to nitrofurantoin	967
<i>nfnB</i>		13	Sensitivity to nitrofurantoin	967
<i>nfo</i>		47	Endonuclease IV	233, W
<i>nfsA</i>	Nitrofuranzone sensitivity	(21)	Nitrofuran reductase I activity	B
<i>nfsB</i>	Nitrofuranzone sensitivity	(11)	Nitrofuran reductase I activity	B
<i>nirB</i>	Nitrate reductase	74	<i>nirD</i> ; NADH-nitrate oxidoreductase (EC 1.6.6.4) aroprotein, structural gene	522, 526, 679, 680
<i>nirC</i>	Nitrate reductase	26	NADH-nitrate reductase (EC 1.6.6.4) activity	B
<i>nmpC</i>	New membrane protein	13	Outer membrane porin protein; locus of <i>qsr</i> prophage	B, 462
<i>non</i>	Nonmucoid	45	Capsule formation	A
<i>nrdA</i>		49	<i>dnaF</i> ; ribonucleoside diphosphate reductase (EC 1.17.4.1) subunit B1	A, B, C, 173, 802, 1118

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>nrdB</i>		49	<i>ftsB</i> ; ribonucleoside diphosphate reductase (EC 1.17.4.1) subunit B1	A, B, C, 173, 593, 1082
<i>nth</i>		36	"Endonuclease III"; a DNA glycosylase and phosphoric monoester lyase	53, 234, 1163
<i>nupC</i>		52	Transport of nucleosides, except guanosine	B, C
<i>nupG</i>		64	Transport of nucleosides	B, 800, 1171
<i>nusA</i>		69	Transcription termination; L factor	B, C, 407, 510, 511, 608, 776, 868, 949
<i>nusB</i>		10	<i>groNB</i> ; transcription termination; L factor	B, C, 509, 1071
<i>nuvA</i>		9	Uridine thiolation factor A activity	B
<i>nuvC</i>		43	Thiazole biosynthesis; 4-thiouridine modification of tRNA; near-UV sensitivity and resistance	940
<i>ompA</i>	Outer membrane protein	22	<i>con</i> , <i>tolG</i> , <i>tut</i> ; outer membrane protein 3a (II*;G;d), structural gene	A, B, C, 207, 403
<i>ompC</i>	Outer membrane protein	48	<i>meoA</i> , <i>par</i> ; outer membrane protein 1b (Ib;c), structural gene	B, C, 745, 746
<i>ompF</i>	Outer membrane protein	21	<i>cmlB</i> , <i>coa</i> , <i>cry</i> , <i>tolF</i> ; outer membrane protein 1a (Ia;b; F), structural gene	B, C, 239, 506, 507, 697, 1085
<i>ompR</i>	Outer membrane protein	75	<i>ompB</i> ; positive regulatory gene for <i>ompC</i> and <i>ompF</i>	B, C, 213, 364, 748, 749, 785, 1191
<i>ompT</i>		13	Outer membrane protein 3b (a), a protease	387, 411, 412, 933
<i>oppA</i>		28	Oligopeptide transport; periplasmic binding protein	A, B, C, 22, 468
<i>oppB</i>		28	Oligopeptide transport	22, 468
<i>oppC</i>		28	Oligopeptide transport	22, 468
<i>oppD</i>		28	Oligopeptide transport	22, 468
<i>oppE</i>		28	Oligopeptide transport	22
<i>opr</i>		(19)	Rate of degradation of aberrant subunit proteins of RNA polymerase	988
<i>ops</i>		63	Level of exopolysaccharide production	1219
<i>optA</i>		4	Deoxyguanosine 5'-triphosphate triphosphohydrolase activity; phage T7 DNA metabolism	C, 72
<i>oriC</i>	Origin of replication	84	<i>poh?</i> ; origin of replication of chromosome	B, C, 152, 542, 578, 712, 819, 820, 987, 1057, 1073, 1152
<i>oriJ</i>	Origin of replication	30	Origin function of <i>rac</i> prophage	C
<i>osmZ</i>		27	<i>bgly</i> , <i>cur</i> , <i>fimG</i> , <i>topX</i> ; DNA supercoiling; expression of genes subject to osmotic regulation	232, 461, 1027
<i>otsA</i>		42	Trehalose phosphate synthase (EC 2.4.1.15) production	374
<i>otsB</i>		42	Trehalose phosphate synthase (EC 2.4.1.15) production	374
<i>pabA</i>	p-Aminobenzoate	74	p-Aminobenzoate synthetase, ColI	A, 555
<i>pabB</i>	p-Aminobenzoate	40	p-Aminobenzoate synthetase, ColI	A, B, 384
<i>pac</i>		31	Phenylacetate degradation	216
<i>panB</i>	Pantothenate	3	Ketopantoate hydroxymethyltransferase (EC 4.1.2.12)	A, B, C
<i>panC</i>	Pantothenate	3	Pantothenate synthetase (EC 6.3.2.1)	A, B, C
<i>panD</i>	Pantothenate	3	Aspartate 1-decarboxylase (EC 4.1.1.11)	A, B, C
<i>panF</i>	Pantothenate	71	Pantothenate permease	1133
<i>pat</i>		89	Putrescine aminotransferase activity	989
<i>pbpA</i>			See <i>mrdA</i>	B, C, 149
<i>pbpB</i>			See <i>ftsI</i>	
<i>pck</i>		75	Phosphoenolpyruvate carboxykinase (EC 4.1.1.49)	C
<i>pcnB</i>		4	Plasmid copy number	666
<i>pcsA</i>		82	Cell division; chromosome segregation	B
<i>pdxA</i>	Pyridoxine	1	Requirement	A, B, C
<i>pdxB</i>	Pyridoxine	50	Placement of 5, 5', and 6' carbons into pyridine ring of pyridoxine	A, B, 30, 31
<i>pdxC</i>			See <i>serC</i>	
<i>pdxH</i>	Pyridoxine	36	Pyridoxinephosphate oxidase	A, B, 415
<i>pdxJ</i>	Pyridoxine	56	Requirement	A, B
<i>pepD</i>	Peptides	6	<i>pepH</i> ; peptidase D, a dipeptidase	A, B, 145, 571
<i>pepN</i>	Peptides	21	Aminopeptidase N	B, C, 55-57, 145, 336, 719-721
<i>pfkA</i>		89	6-Phosphofructokinase I (EC 2.7.1.11)	A, B, 240, 456
<i>pfkB</i>		38	Level of 6-phosphofructokinase II; suppressor of <i>pfkA</i>	A, B, C, 241
<i>pfl</i>		20	Pyruvate formate-lyase	B, 839
<i>pgi</i>		91	Glucosephosphate isomerase (EC 5.3.1.9)	A, N
<i>pgk</i>		63	Phosphoglycerate kinase (EC 2.7.2.3)	A, B

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>pgl</i>		17	<i>blu</i> ; 6'-phosphogluconolactonase (EC 3.1.1.31)	A
<i>pgm</i>		(15)	Phosphoglucomutase (EC 2.7.5.1)	A
<i>pgpA</i>		10	Phosphatidylglycerophosphate phosphatase, membrane bound	500
<i>pgpB</i>		28	Phosphatidylglycerophosphate phosphatase, membrane bound	500
<i>pgsA</i>		42	Phosphatidylglycerophosphate synthetase (EC 2.7.8.5)	A, B, C, 386
<i>pgsB</i>			See <i>lpxB</i>	
<i>pheA</i>	Phenylalanine	57	Chorismate mutase-P-prephenate dehydrogenase	A, B, C, 488
<i>pheP</i>	Phenylalanine	13	Phenylalanine-specific transport system	C, 395
<i>pheR</i>	Phenylalanine	94	Regulatory gene for <i>pheA</i>	A, B, C, 306, 320, 727, 728, 867, 1035, 1036, 1190
<i>pheS</i>	Phenylalanine	37	<i>phe-act</i> ; phenylalanyl-tRNA synthetase (EC 6.1.1.20), α subunit	A, B, C, 306, 320, 727, 728, 867, 1035, 1190
<i>pheT</i>	Phenylalanine	37	<i>pheS</i> ; phenylalanyl-tRNA synthetase (EC 6.1.1.20), β subunit	A, B, C, 306, 320, 727, 728, 867, 1035, 1190
<i>pheU</i>	Phenylalanine	94	Phenylalanyl-tRNA (duplicate gene)	357, 587, 976
<i>pheV</i>	Phenylalanine	64	Phenylalanyl-tRNA (duplicate gene)	166, 587, 1179
<i>phnD</i>		92	<i>psiD</i> ; carbon-phosphorus lyase	1148, U
<i>phoA</i>	Phosphate	9	Alkaline phosphatase (EC 3.1.3.1)	A, B, C, 184, 1011
<i>phoB</i>	Phosphate	9	<i>phoRc</i> , <i>phoT</i> ; positive regulatory gene for <i>pho</i> regulon	A, B, C, 691, 693, 695, 1006, 1157
<i>phoE</i>	Phosphate	6	<i>ompE</i> ; outer membrane pore protein e (E,Ic,NmpAB), structural gene	C, 450, 810, 827, 1106
<i>phoM</i>	Phosphate	100	Positive regulatory gene for <i>pho</i> regulon	C, 17, 671, 694, 695, 1105, 1156, 1159
<i>phoR</i>	Phosphate	9	<i>nmpB</i> , <i>phoR1</i> , <i>R1pho</i> ; positive and negative regulatory gene for <i>pho</i> regulon	A, B, C, 692, 695, 1006, 1157
<i>phoS</i>	Phosphate	84	See <i>pstS</i>	
<i>phoT</i>	Phosphate	84	See <i>pstA</i> , <i>pstB</i> , and <i>phoU</i>	
<i>phoU</i>	Phosphate	84	<i>phoT</i> ; high-affinity phosphate-specific transport system, regulatory gene	C, 16, 18, 779, 1065
<i>phr</i>	Photoreactivation	16	Deoxyribodipyrimidine photolyase (EC 4.1.99.3)	A, B, 495, 957, 958
<i>phxB</i>	Phi-X	17	Adsorption of ϕ X174	B
<i>pil</i>	Pili	98	See <i>fim</i>	
<i>pin</i>		26	Inversion of adjacent DNA; locus of element e14	312, 563, 861, 862, 1139, L
<i>pit</i>	P _i transport	77	Low-affinity P _i transport	A, 308, 309
<i>pldA</i>		86	Detergent-resistant phospholipase A	A, 14, 263, 264, 471, 472, 579
<i>pldB</i>		86	Lysophospholipase L ₂	14, 472, 579, 580
<i>plsA</i>	Phospholipid synthesis	11	See <i>adk</i>	
<i>plsB</i>	Phospholipid synthesis	92	Glycerolphosphate acyltransferase activity	A, B, C, 646
<i>plsX</i>	Phospholipid synthesis	24	Glycerolphosphate auxotrophy in <i>plsB</i> background	620
<i>pncA</i>	Pyridine nucleotide cycle	39	<i>nam</i> ; nicotinamide deamidase (EC 3.5.1.19)	A, B
<i>pncB</i>	Pyridine nucleotide cycle	(21)	Nicotinate phosphoribosyltransferase (EC 2.4.2.11)	C
<i>pnp</i>		69	Polynucleotide phosphorylase (EC 2.7.7.8)	A, C, 227, 318, 470, 873, 897, 898, 1078
<i>pntA</i>		35	Pyridine nucleotide transhydrogenase (EC 1.6.1.1), α subunit	B, 197, 198
<i>pntB</i>		35	Pyridine nucleotide transhydrogenase (EC 1.6.1.1), β subunit	197, 198
<i>poaR</i>		63	Regulation of proline oxidase production	A
<i>pog</i>		70	Growth of phage P1	C
<i>polA</i>	Polymerase	87	<i>resA</i> ; DNA polymerase I (EC 2.7.7.7)	A, B, C
<i>polB</i>	Polymerase	2	DNA polymerase II (EC 2.7.7.7)	A
<i>polC</i>	Polymerase	4	<i>dnaE</i> ; DNA biosynthesis; DNA polymerase III α subunit	A, B, C, 998, 1103, 1168
<i>popC</i>	Porphyrin	4	Synthesis of δ -aminolevulinate	A
<i>popD</i>	Porphyrin	(1)	Level of 5-aminolevulinate dehydratase (EC 4.2.1.24) activity	A, B
<i>poxA</i>		95	Regulatory gene for <i>poxB</i>	C
<i>poxB</i>		19	Pyruvate oxidase (EC 1.2.2.2), structural gene	C, 185, 396, 397
<i>ppc</i>	Phosphoenolpyruvate	89	<i>glu</i> , <i>asp</i> ; phosphoenolpyruvate carboxylase (EC 4.1.1.31)	A, B, C, 354, 943
<i>pps</i>	Phosphoenolpyruvate	37	Phosphoenolpyruvate synthase	A
<i>prfA</i>		27	<i>asuA?</i> , <i>sueB</i> , <i>uar</i> , <i>ups?</i> ; protein release factor 1	174, 941, 942
<i>prfB</i>		62	<i>supK</i> ; protein release factor 2	564

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>prlA</i>		73	<i>secY</i> ; protein export; membrane protein	10, 181, 311, 516, 517, 1002, 1009
<i>prlB</i>		85	Protein export	311
<i>prlC</i>		71	Protein export	311
<i>prlD</i>		2	Protein export	60
<i>prmA</i>		71	<i>prm-1</i> ; methylation of 50S ribosomal subunit protein L11	B
<i>prmB</i>		51	<i>prm-2</i> ; methylation of 50S ribosomal subunit protein L3	B
<i>proA</i>	Proline	6	<i>prol</i> ; γ -glutamyl phosphate reductase (EC 1.2.1.41)	A, C, 272, 450, 687, 797
<i>proB</i>	Proline	6	<i>pro2</i> ; γ -glutamyl kinase (EC 2.7.2.11)	A, C, 272, 450, 687, 797
<i>proC</i>	Proline	9	<i>pro3</i> , <i>pro2</i> ; pyrrolidine-5-carboxylate reductase (EC 1.5.1.2)	A, C, 262, 273
<i>proK</i>	Proline	80	<i>proV</i> ; proline tRNA 1	341, 587, 599
<i>proL</i>	Proline	47	<i>proW</i> ; proline tRNA 2	587
<i>proM</i>	Proline	86	<i>proU</i> ; proline tRNA 3	587
<i>proP</i>	Proline	93	Low-affinity transport system for glycine betaine and proline; proline permease II	C, 392, 393, 716
<i>proS</i>	Proline	5	Prolyl-tRNA synthetase (EC 1.1.1.15)	C
<i>proT</i>	Proline	83	Proline transport	B, C
<i>proU</i>	Proline	57	<i>osrA</i> ; high-affinity transport system for glycine betaine and proline	319, 392, 394, 418, 716, I
<i>proV</i>	Proline	57	High-affinity transport system for glycine betaine and proline; glycine betaine-binding protein	319, 341, 394, I
<i>proW</i>	Proline	57	High-affinity transport system for glycine betaine and proline	I
<i>ppr</i>	Propionate	97	Propionate metabolism	C
<i>ppr</i>		31	γ -Aminobutyraldehyde (pyrroline) dehydrogenase activity	989
<i>prs</i>		26	Phosphoribosylpyrophosphate synthetase (EC 2.7.6.1)	C, 480–482
<i>psd</i>		95	Phosphatidylserine decarboxylase	A, B
<i>psiF</i>		9	Induced by phosphate starvation	184, 1158, U
<i>pssA</i>		56	Phosphatidylserine synthetase (EC 2.7.8.8)	B, C
<i>pssR</i>		85	Regulatory gene	1026
<i>pstA</i>		84	<i>phoR2b</i> , <i>phoT</i> , <i>R2pho</i> ; high-affinity phosphate-specific transport system	A, B, C, 16, 18, 922, 1066
<i>pstB</i>		84	<i>phoT</i> ; high-affinity phosphate-specific transport system, cytoplasmic membrane protein?	A, B, C, 16, 18, 638, 922, 1066
<i>pstC</i>		84	<i>phoW</i> ; high-affinity phosphate-specific transport system, cytoplasmic membrane component	A, B, C, 16, 18, 922, 1066
<i>pstS</i>		84	<i>nmpA</i> , <i>phoR2a</i> , <i>phoS</i> , <i>R2pho</i> ; high-affinity phosphate-specific transport system; periplasmic phosphate-binding protein	A, B, C, 16, 18, 146, 520, 639, 683, 754, 922, 1065, 1066
<i>pta</i>		50	Phosphotransacetylase (EC 2.3.1.8) activity	B, C
<i>pth</i>		26	Peptidyl-tRNA hydrolase	A
<i>ptr</i>		61	Protease III	C, 61, 200, 295, 296, 330
<i>ptsG</i>	Phosphotransferase system	25	<i>car</i> , <i>CR</i> , <i>gpt</i> , <i>gptA</i> , <i>tgl</i> , <i>umg</i> ; glucosphingophotransferase enzyme II	A, B, 123, 314
<i>ptsH</i>	Phosphotransferase system	52	<i>ctr</i> , <i>Hpr</i> ; phosphohistidinoprotein-hexose phosphotransferase (EC 2.7.1.69)	A, B, 134–136, 270, 271, 835, 945
<i>ptsI</i>	Phosphotransferase system	52	<i>ctr</i> ; phosphotransferase system enzyme I	A, B, 134–136, 270, 271, 835, 945
<i>purA</i>	Purine	95	<i>ade₁</i> ; <i>Ad₄</i> ; adenylosuccinate synthetase (EC 6.3.4.4)	A
<i>purB</i>	Purine	25	<i>ade₁</i> ; adenylosuccinate lyase (EC 4.3.2.2)	A, L
<i>purC</i>	Purine	53	<i>ade₈</i> ; phosphoribosylaminoimidazole-succinocarboxamide synthetase (EC 6.3.2.6)	A, 833
<i>purD</i>	Purine	90	<i>adth_a</i> ; phosphoribosylglycineamide synthetase (EC 6.3.4.13)	A
<i>purE</i>	Purine	12	<i>ade₂</i> , <i>ade_f</i> , <i>Pur₂</i> ; phosphoribosylaminoimidazole carboxylase (EC 4.1.1.21), catalytic subunit	A, C, 548, 1095
<i>purF</i>	Purine	50	<i>ade_{u,b}</i> , <i>purC</i> ; amidophosphoribosyl transferase (EC 2.4.2.14)	A, C, 689, 807
<i>purG</i>	Purine		See <i>purM</i>	
<i>purH</i>	Purine	90	<i>ade_i</i> , <i>purJ</i> ; phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3)	A
<i>purI</i>	Purine		See <i>purL</i>	
<i>purK</i>	Purine	12	<i>purE₂</i> ; phosphoribosylaminoimidazole carboxylase (EC 4.1.1.21), CO ₂ -fixing subunit	548, 1095

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>purL</i>	Purine	55	<i>purl</i> ; phosphoribosylformylglycineamide synthetase (EC 6.3.5.3); homologous to <i>purG</i> of <i>S. typhimurium</i>	A, C, 479
<i>purM</i>	Purine		<i>purG</i> ; phosphoribosylaminoimidazole synthetase (EC 6.3.3.1) homologous to <i>purL</i> of <i>S. typhimurium</i>	A, B, C, 479, 1022, 1023
<i>purN</i>	Purine	54	<i>ade</i> ; 5'-phosphoribosylglycinamide transformylase (EC 2.1.2.2)	1023
<i>purP</i>	Purine	84	High-affinity adenine transport	156, E
<i>purR</i>	Purine	36	Regulatory gene for <i>pur</i> regulon	568, 919, S
<i>pus</i>		20	Effect of suppressors on <i>relB</i> mutations	C
<i>putA</i>	Proline utilization	23	<i>poaA</i> ; proline dehydrogenase (EC 1.5.99.8)	A, C, 752, 778
<i>putP</i>	Proline utilization	23	Proline utilization; major proline permease	C, 752, 777, 778
<i>pykF</i>		37	Pyruvate kinase F	365
<i>pyrA</i>	Pyrimidine	1	See <i>car</i>	
<i>pyrB</i>	Pyrimidine	97	Aspartate carbamoyltransferase (EC 2.1.3.2) catalytic subunit	A, B, C, 474, 578, 637, 789, 838, 921, 1119
<i>pyrC</i>	Pyrimidine	24	Dihydroorotase (EC 3.5.2.3)	A, 48, 530, 1178
<i>pyrD</i>	Pyrimidine	21	Dihydroorotid oxidase (EC 1.3.3.1)	A, 530, 618
<i>pyrE</i>	Pyrimidine	82	Orotate phosphoribosyltransferase (EC 2.4.2.10)	A, C, 876, 877
<i>pyrF</i>	Pyrimidine	28	Orotidine-5'-phosphate decarboxylase (EC 4.1.1.23)	A, 282, 530, 1120
<i>pyrG</i>	Pyrimidine	60	CTP synthetase (EC 6.3.4.2)	B, C, 1169
<i>pyrH</i>	Pyrimidine	5	UMP kinase	A
<i>pyrI</i>	Pyrimidine	97	Aspartate carbamoyltransferase (EC 2.1.3.2) regulatory subunit	C, 474, 838, 921
<i>pyrS</i>	Pyrimidine	81	Regulatory gene	809
<i>qin</i>		35	<i>kim</i> ; cryptic lambdoid phage	122, 316
<i>qmeA</i>		29	<i>gts</i> ; unspecified membrane defect	A
<i>qmeC</i>		74	Unspecified membrane defect; tolerance to glycine, penicillin sensitivity	A
<i>qmeD</i>		61	Unspecified membrane defect; tolerance to glycine, penicillin sensitivity	A
<i>qmeE</i>		37	Unspecified membrane defect	A
<i>qsr'</i>		13	Cryptic lambdoid phage	23, 109, 462, 545
<i>rac</i>		30	Defective prophage <i>rac</i> ; see <i>recE</i> and <i>oriJ</i>	A, C, 1176, 1177
<i>radA</i>		100	Sensitivity to γ and UV radiation and methyl methanesulfonate	280
<i>radC</i>		82	Sensitivity to radiation	A, 322
<i>ranA</i>		56	RNA metabolism	A
<i>rap</i>		26	Growth of phage lambda	419
<i>ras</i>	Radiation sensitivity	(10)	Sensitivity to UV and X-rays	A
<i>rbsA</i>	Ribose	84	<i>rbsP</i> , <i>rbsT</i> ; D-ribose high-affinity transport system; membrane-associated protein	85, 502, 667
<i>rbsB</i>	Ribose	84	<i>rbsP</i> ; D-ribose periplasmic binding protein	502, 667
<i>rbsC</i>	Ribose	84	<i>rbsP</i> , <i>rbsT</i> ; D-ribose high-affinity transport system; membrane-associated protein	85, 502, 667
<i>rbsD</i>	Ribose	84	<i>rbsP</i> ; D-ribose high-affinity transport system; membrane-associated protein	85
<i>rbsK</i>	Ribose	84	Ribokinase (EC 2.7.1.15)	A, B, C, 475, 502, 667
<i>rbsR</i>	Ribose	84	Regulatory gene	667
<i>rcsA</i>		43	Positive regulatory gene for capsule synthesis	390, 1107
<i>rcsB</i>		48	Positive regulatory gene for capsule synthesis	133, 390
<i>rcsC</i>		48	Negative regulatory gene for capsule synthesis	133, 390
<i>rdgA</i>		16	Dependence of growth upon <i>recA</i> gene product	C
<i>rdgB</i>		64	Dependence of growth and viability upon <i>recA</i> function	204
<i>recA</i>	Recombination	58	<i>lexB</i> , <i>recH</i> , <i>rnmB</i> , <i>tif</i> , <i>umuB</i> , <i>zab</i> ; general recombination, DNA repair and induction of phage lambda	A, B, C
<i>recB</i>	Recombination	61	<i>rorA</i> ; recombination and DNA repair; exonuclease V (EC 3.1.11.5)	A, B, C, 296, 329, 965
<i>recC</i>	Recombination	61	Recombination and DNA repair; exonuclease V (EC 3.1.11.5)	A, B, C, 296, 331, 333, 965
<i>recD</i>	Recombination	61	Recombination and DNA repair; exonuclease V (EC 3.1.11.5), α subunit	19, 94, 328
<i>recE</i>	Recombination	30	<i>rac</i> ; locus of <i>rac</i> prophage; recombination and DNA repair; exonuclease VIII	A, B, C, 342, 1177
<i>recF</i>	Recombination	83	<i>uvrF</i> ; recombination and DNA repair	A, B, C, 4, 27, 100, 894
<i>recJ</i>	Recombination	62	Recombination and DNA repair	668, 669
<i>recN</i>	Recombination	57	<i>radB</i> ; recombination and DNA repair	658, 851, 926, 963, 964

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>recO</i>	Recombination	56	Conjugational recombination and DNA repair	585
<i>recQ</i>	Recombination	86	Conjugational recombination and DNA repair	14, 508, 781, 782
<i>relA</i>	Relaxed	60	<i>RC</i> ; regulation of RNA synthesis; stringent factor; ATP:GTP 3'-pyrophosphotransferase	A, B
<i>relB</i>	Relaxed	35	Regulation of RNA synthesis	B, C, 74
<i>relE</i>	Relaxed	35	Locus in <i>relB</i> operon; function unknown	74, 372
<i>relF</i>	Relaxed	35	Locus in <i>relB</i> operon; function unknown	74, 372
<i>relX</i>	Relaxed	60	Control of synthesis of guanosine-5'-diphosphate-3'-diphosphate	B
<i>rep</i>		85	<i>dasC?</i> , <i>mmrA?</i> ; Rep helicase, a single-stranded DNA dependent ATPase	A, B, C, 14, 70, 92, 93, 285, 376
<i>rer</i>		90	Resistance to UV and γ -radiation	B
<i>rfa</i>	Rough	81	<i>con</i> , <i>lpsA</i> , <i>phx</i> ; cluster of genes coding for enzymes involved in lipopolysaccharide core biosynthesis	A, B
<i>rfaB</i>	Rough	81	UDP-D-galactose:(glucosyl)lipopolysaccharide-1,6-D-galactosyltransferase	226
<i>rfaC</i>	Rough	81	Lipopolysaccharide core biosynthesis; proximal hexose	C
<i>rfaD</i>	Rough	81	ADP-L-Glycero-D-mannoheptose-6-epimerase	C, 211
<i>rfaG</i>	Rough	81	Lipopolysaccharide core biosynthesis; glucosyltransferase I	226
<i>rfaH</i>	Rough	87	<i>sfrB</i> ; lipopolysaccharide core biosynthesis; positive regulation of production of glucosyltransferase; expression of <i>tra</i> operon of F factor; antiterminator	226, 900
<i>rfaI</i>	Rough	81	UDP-D-galactose:(glucosyl)lipopolysaccharide- α -1,3-D-galactosyltransferase	226
<i>rfaJ</i>	Rough	81	UDP-D-glucose:(galactosyl)lipopolysaccharide glucosyltransferase	226
<i>rfaM</i>	Rough	81	Lipopolysaccharide core biosynthesis; glucosyltransferase II	226
<i>rfaP</i>	Rough	81	Lipopolysaccharide core biosynthesis; phosphorylation of core heptose	C
<i>rfbA</i>	Rough	45	TDP-glucose pyrophosphorylase	A
<i>rfbB</i>	Rough	45	TDP-glucose oxidoreductase	A
<i>rfbD</i>	Rough	45	TDP-rhamnose synthetase	A
<i>rfe</i>	Rough	(85)	Synthesis of enterobacterial common antigen and O antigen	B, 731
<i>rff</i>	Rough	(85)	Synthesis of enterobacterial common antigen	B, 731
<i>rhaA</i>	Rhamnose	88	L-Rhamnose isomerase (EC 5.3.1.14)	A, 1101
<i>rhaB</i>	Rhamnose	88	Rhamnulokinase (EC 2.7.1.5)	A, 1101
<i>rhaD</i>	Rhamnose	88	Rhamnulose-1-phosphate aldolase (EC 4.1.2.19)	A, 1101
<i>rhaR</i>	Rhamnose	88	<i>rhaC</i> ; positive regulatory gene	1101
<i>rhaS</i>	Rhamnose	88	<i>rhaC</i> ; positive regulatory gene	1101
<i>rho</i>		85	<i>nitA</i> , <i>psu</i> , <i>rncC</i> , <i>SuA</i> , <i>sun</i> , <i>tsu</i> ; transcription termination factor rho; polarity suppressor	A, B, C, 14, 70, 143, 167, 650, 713, 857
<i>RhsA</i>		81	Repetitive sequence responsible for duplications within chromosome	652, 944
<i>RhsB</i>		77	Repetitive sequence responsible for duplications within chromosome	652, 944
<i>RhsC</i>		16	Repetitive sequence responsible for duplications within chromosome	944
<i>RhsD</i>		12	Repetitive sequence responsible for duplications within chromosome	944
<i>ribA</i>	Riboflavin	28	GTP cyclohydrolase II	C, 58, 1088
<i>ribB</i>	Riboflavin	66	Block before 6,7-dimethyl-8-ribityllumazine	C, 58, 1088
<i>ribC</i>	Riboflavin	40	Riboflavin synthase	58, 1088, R
<i>ridA</i>		71	Transcription and translation; rifampin and kasugamycin dependence	C
<i>ridB</i>		85	Transcription and translation; rifampin dependence	236
<i>rimB</i>	Ribosomal modification	38	Maturation of 50S ribosomal subunit	A, 415
<i>rimC</i>	Ribosomal modification	(26)	Maturation of 50S ribosomal subunit	A
<i>rimD</i>	Ribosomal modification	(88)	Maturation of 50S ribosomal subunit	A
<i>rimE</i>	Ribosomal modification	72	Modification of ribosomal proteins	B, 730
<i>rimF</i>	Ribosomal modification	1	<i>res</i> ; ribosomal modification	A
<i>rimG</i>	Ribosomal modification	(1)	<i>ramB</i> ; modification of 30S ribosomal subunit protein S4	A
<i>rimH</i>	Ribosomal modification	14	<i>stsB</i> ; ribosomal modification	A, B

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>rimI</i>	Ribosomal modification	99	Modification of 30S ribosomal subunit protein S18; acetylation of N-terminal alanine	B, C, 1209
<i>rimJ</i>	Ribosomal modification	(32)	Modification of 30S ribosomal subunit protein S5; acetylation of N-terminal alanine	B, 524, 1209
<i>rimL</i>	Ribosomal modification	(33)	Modification of 30S ribosomal subunit protein L7; acetylation of N-terminal serine	C
<i>rit</i>		89	Affects thermolability of 50S ribosomal subunit	B
<i>rlpA</i>		15	A minor lipoprotein	1076
<i>rlpB</i>		15	A minor lipoprotein	1076
<i>rna</i>	RNAse	14	<i>rns</i> , <i>rnsA</i> ; RNAse I	A
<i>rnb</i>	RNAse	29	RNAse II	B, C
<i>rnc</i>	RNAse	55	RNAse III	A, B, 699, 787, 1160
<i>rnd</i>	RNAse	40	RNAse D	C, 1216
<i>rne</i>	RNAse	24	RNAse E activity	B, C, 893
<i>rnh</i>	RNAse	5	<i>dasF</i> , <i>herA</i> , <i>sdrA</i> , <i>sin</i> ; RNAse H (EC 3.1.26.4)	C, 225, 550, 690, 771, 806, 813, 1108
<i>rnpA</i>	RNAse	83	RNAse P, protein component	435
<i>rnpB</i>	RNAse	70	RNAse P, RNA subunit, M1 RNA	B, C, 758, 895, 896, 952
<i>rodA</i>		15	See <i>mrdB</i>	
<i>rpiA</i>		63	Ribose phosphate isomerase (EC 5.3.1.6), constitutive	A
<i>rplA</i>	Ribosomal protein, large	90	50S ribosomal subunit protein L1	A, B, C, 283, 491, 889
<i>rplB</i>	Ribosomal protein, large	73	50S ribosomal subunit protein L2	A, B, 1222
<i>rplC</i>	Ribosomal protein, large	73	50S ribosomal subunit protein L3	A, B, 1222
<i>rplD</i>	Ribosomal protein, large	73	<i>eryA</i> ; 50S ribosomal subunit protein L4	A, B, C, 1222
<i>rplE</i>	Ribosomal protein, large	73	50S ribosomal subunit protein L5	A, B, 181
<i>rplF</i>	Ribosomal protein, large	73	50S ribosomal subunit protein L6	A, B, 181
<i>rplI</i>	Ribosomal protein, large	96	50S ribosomal subunit protein L9	B, 974
<i>rplJ</i>	Ribosomal protein, large	90	50S ribosomal subunit protein L10	A, B, C, 203, 283, 491, 889
<i>rplK</i>	Ribosomal protein, large	90	<i>relC</i> ; 50S ribosomal subunit protein L11	A, B, C, 283, 491, 889
<i>rplL</i>	Ribosomal protein, large	90	50S ribosomal subunit protein L7/L12	A, B, C, 283, 491, 889
<i>rplM</i>	Ribosomal protein, large	70	50S ribosomal subunit protein L13	C, 514
<i>rplN</i>	Ribosomal protein, large	73	50S ribosomal subunit protein L14	A, B, 181
<i>rplO</i>	Ribosomal protein, large	73	50S ribosomal subunit protein L15	A, B, 181, 516
<i>rplP</i>	Ribosomal protein, large	73	50S ribosomal subunit protein L16	A, B, 1222
<i>rplQ</i>	Ribosomal protein, large	73	50S ribosomal subunit protein L17	A, B, C, 77, 181, 730
<i>rplR</i>	Ribosomal protein, large	73	50S ribosomal subunit protein L18	A, B, 181
<i>rplS</i>	Ribosomal protein, large	57	50S ribosomal subunit protein L19	B, 164
<i>rplT</i>	Ribosomal protein, large	38	<i>pdzA</i> ; 50S ribosomal subunit protein L20	320
<i>rplU</i>	Ribosomal protein, large	69	50S ribosomal subunit protein L21	B
<i>rplV</i>	Ribosomal protein, large	73	50S ribosomal subunit protein L22	A, B, 1222
<i>rplW</i>	Ribosomal protein, large	73	50S ribosomal subunit protein L23	B, 1222
<i>rplX</i>	Ribosomal protein, large	73	50S ribosomal subunit protein L24	A, B, 181, 235
<i>rplY</i>	Ribosomal protein, large	48	50S ribosomal subunit protein L25	B
<i>rpmA</i>	Ribosomal protein, large	69	50S ribosomal subunit protein L27	B
<i>rpmB</i>	Ribosomal protein, large	82	50S ribosomal subunit protein L28	B, C, 1031
<i>rpmC</i>	Ribosomal protein, large	73	50S ribosomal subunit protein L29	A, B, 1222
<i>rpmD</i>	Ribosomal protein, large	73	50S ribosomal subunit protein L30	A, B, 181
<i>rpmE</i>	Ribosomal protein, large	89	50S ribosomal subunit protein L31	C
<i>rpmF</i>	Ribosomal protein, large	24	50S ribosomal subunit protein L32	524
<i>rpmG</i>	Ribosomal protein, large	82	50S ribosomal subunit protein L33	B, C, 1031
<i>rpmH</i>	Ribosomal protein, large	83	<i>rimA</i> , <i>ssaF</i> ; 50S ribosomal subunit protein L34	C, 823, O
<i>rpmI</i>	Ribosomal protein, large	38	50S ribosomal subunit protein A	1149
<i>rpmJ</i>	Ribosomal protein, large	73	50S ribosomal subunit protein X	181, 1149
<i>rpoA</i>	RNA polymerase	73	RNA polymerase (EC 2.7.7.6), α subunit	A, B, C, 77, 181, 730, 928, 929
<i>rpoB</i>	RNA polymerase	90	<i>groN</i> , <i>nitB</i> , <i>rif</i> , <i>ron</i> , <i>stl</i> , <i>stv</i> , <i>tabD</i> ; RNA polymerase (EC 2.7.7.6), β subunit	A, B, C, 283, 491, 889
<i>rpoC</i>	RNA polymerase	90	<i>tabD</i> ; RNA polymerase (EC 2.7.7.6), β subunit	A, B, C, 283, 889
<i>rpoD</i>	RNA polymerase	67	<i>alt</i> ; RNA polymerase (EC 2.7.7.6), σ^{70} subunit	B, C, 157, 677, 1086
<i>rpoH</i>	RNA polymerase	76	<i>fam</i> , <i>hin</i> , <i>htpR</i> ; RNA polymerase (EC 2.7.7.6), σ^{32} subunit; regulatory gene for proteins induced at high temperatures	C, 416, 417, 614, 792, 1098, 1116, 1213
<i>rpoN</i>	RNA polymerase	70	<i>glnF</i> , <i>ntrA</i> ; RNA polymerase (EC 2.7.7.6), σ^{60} subunit	B, C, 70, 177, 467, 494
<i>rpsA</i>	Ribosomal protein, small	21	<i>ssyF</i> ; 30S ribosomal subunit protein S1	B, C, 291, 841, 1001
<i>rpsB</i>	Ribosomal protein, small	4	30S ribosomal subunit protein S2	A, B, C

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>rpsC</i>	Ribosomal protein, small	73	30S ribosomal subunit protein S3	A, B, 1222
<i>rpsD</i>	Ribosomal protein, small	73	<i>ramA</i> ; <i>sud2</i> ; 30S ribosomal subunit protein S4	A, B, C, 77, 181
<i>rpsE</i>	Ribosomal protein, small	73	<i>eps</i> , <i>spcA</i> , <i>spc</i> ; 30S ribosomal subunit protein S5	A, B, 181
<i>rpsF</i>	Ribosomal protein, small	95	30S ribosomal subunit protein S6	A, B, 974
<i>rpsG</i>	Ribosomal protein, small	73	<i>K12</i> ; 30S ribosomal subunit protein S7	A, B, C
<i>rpsH</i>	Ribosomal protein, small	73	30S ribosomal subunit protein S8	A, B, 181
<i>rpsI</i>	Ribosomal protein, small	70	30S ribosomal subunit protein S9	237, 514
<i>rpsJ</i>	Ribosomal protein, small	73	30S ribosomal subunit protein S10	A, B, C
<i>rpsK</i>	Ribosomal protein, small	73	30S ribosomal subunit protein S11	A, B, C, 77, 181
<i>rpsL</i>	Ribosomal protein, small	73	<i>strA</i> ; 30S ribosomal subunit protein S12	A, B, C
<i>rpsM</i>	Ribosomal protein, small	73	30S ribosomal subunit protein S13	A, B, C, 77, 181
<i>rpsN</i>	Ribosomal protein, small	73	30S ribosomal subunit protein S14	A, B, 181
<i>rpsO</i>	Ribosomal protein, small	69	<i>secC</i> ; 30S ribosomal subunit protein S15	B, C, 318, 324, 873, 898, 903, 1077, 1078, H
<i>rpsP</i>	Ribosomal protein, small	57	30S ribosomal subunit protein S16	B, 164
<i>rpsQ</i>	Ribosomal protein, small	73	<i>neaA</i> ; 30S ribosomal subunit protein S17	A, B, 1222
<i>rpsR</i>	Ribosomal protein, small	96	30S ribosomal subunit protein S18	A, B, 974
<i>rpsS</i>	Ribosomal protein, small	73	30S ribosomal subunit protein S19	A, B, 1222
<i>rpsT</i>	Ribosomal protein, small	0	<i>supS20</i> ; 30S ribosomal subunit protein S20	A, B, 681, 1196
<i>rpsU</i>	Ribosomal protein, small	67	30S ribosomal subunit protein S21	B, C, 157, 677
<i>rrfA</i>	rRNA 5S	87	5S rRNA gene of <i>rrnA</i> operon	B, C
<i>rrfB</i>	rRNA 5S	90	5S rRNA gene of <i>rrnB</i> operon	B, C
<i>rrfC</i>	rRNA 5S	85	5S rRNA gene of <i>rrnC</i> operon	B, C
<i>rrfD</i>	rRNA 5S	72	5S rRNA gene of <i>rrnD</i> operon	C
<i>rrfE</i>	rRNA 5S	90	5S rRNA gene of <i>rrnE</i> operon	B, C
<i>rrfG</i>	rRNA 5S	56	5S rRNA gene of <i>rrnG</i> operon	C
<i>rrfH</i>	rRNA 5S	5	5S rRNA gene of <i>rrnH</i> operon	C
<i>rrlA</i>	rRNA, 23S	87	23S rRNA gene of <i>rrnA</i> operon	A, B, C
<i>rrlB</i>	rRNA, 23S	90	23S rRNA gene of <i>rrnB</i> operon	B, C
<i>rrlC</i>	rRNA, 23S	85	23S rRNA gene of <i>rrnC</i> operon	B
<i>rrlD</i>	rRNA, 23S	72	23S rRNA gene of <i>rrnD</i> operon	B, C
<i>rrlE</i>	rRNA, 23S	90	23S rRNA gene of <i>rrnE</i> operon	B, C
<i>rrlG</i>	rRNA, 23S	56	23S rRNA gene of <i>rrnG</i> operon	B, C
<i>rrlH</i>	rRNA, 23S	5	23S rRNA gene of <i>rrnH</i> operon	C
<i>rrnA</i>	rRNA	87	<i>cqsA</i> ; rRNA operon	A, B, C, 578
<i>rrnB</i>	rRNA	90	<i>cqsE</i> , <i>rrnB1</i> ; rRNA operon	A, B, C, 89, 446
<i>rrnC</i>	rRNA	85	<i>cqsB</i> , <i>rrnB</i> , <i>rrnB2</i> ; rRNA operon	A, B, C, 446, 578
<i>rrnD</i>	rRNA	72	<i>cqsD</i> ; rRNA operon	B, C
<i>rrnE</i>	rRNA	90	<i>rrnD1</i> ; rRNA operon	B, C, 645
<i>rrnG</i>	rRNA	56	rRNA operon	B, C, 446
<i>rrnH</i>	rRNA	5	rRNA operon	C
<i>rrsA</i>	rRNA, 16S	87	16S rRNA gene of <i>rrnA</i> operon	B
<i>rrsB</i>	rRNA, 16S	90	16S rRNA gene of <i>rrnB</i> operon	B, C, 89, 121
<i>rrsC</i>	rRNA, 16S	85	16S rRNA gene of <i>rrnC</i> operon	B
<i>rrsD</i>	rRNA, 16S	72	16S rRNA gene of <i>rrnD</i> operon	B
<i>rrsE</i>	rRNA, 16S	90	16S rRNA gene of <i>rrnE</i> operon	B
<i>rrsG</i>	rRNA, 16S	56	16S rRNA gene of <i>rrnG</i> operon	B, C
<i>rrsH</i>	rRNA, 16S	5	16S rRNA gene of <i>rrnH</i> operon	C
<i>rts</i>		90	<i>ts-9</i> ; uncharacterized growth defect	A, B, C, 1079
<i>ruvA</i>		41	Filament formation and sensitivity to UV radiation	A, 37, 87, 1010
<i>ruvB</i>		41	Filament formation and sensitivity to UV radiation	87
<i>sad</i>		34	Succinate-semialdehyde dehydrogenase (EC 1.2.1.16), NAD dependent	C, 702
<i>sbaA</i>		97	Regulation of serine and branched-chain amino acid metabolism	C
<i>sbcB</i>		44	<i>xonA</i> ; exonuclease I; suppression of <i>recB</i> <i>recC</i> mutations	A, 846, 847, 879
<i>sbcC</i>		9	Suppression of <i>recB</i> <i>recC</i> mutations	657
<i>sbp</i>		89	Periplasmic sulfate-binding protein	456
<i>sbmA</i>		9	Sensitivity to microcin B17	622
<i>sdhA</i>		16	Succinate dehydrogenase (EC 1.3.99.1), flavoprotein subunit	A, C, 247, 1174, 1184
<i>sdhB</i>		16	Succinate dehydrogenase (EC 1.3.99.1), iron sulfur protein	A, C, 247, 1174, 1184
<i>sdhC</i>		16	<i>cytB</i> ; succinate dehydrogenase (EC 1.3.99.1), cytochrome <i>b</i> ₅₅₆	A, C, 763, 764

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>sdhD</i>		16	Succinate dehydrogenase (EC 1.3.99.1), hydrophobic subunit	A, C, 1174, 1184
<i>secA</i>		2	<i>azi, pea</i> ; secretion of envelope proteins	C, 71, 972, O
<i>secB</i>		81	Protein export	600, 601
<i>secD</i>		9	Protein export	361
<i>sefA</i>		4	Septum formation	B
<i>selA</i>	Selenium	81	<i>fdhA</i> ; selenium metabolism; biosynthesis or incorporation of selenocystein	632
<i>selB</i>	Selenium	81	<i>fdhA</i> ; selenium metabolism; biosynthesis or incorporation of selenocystein	632
<i>selC</i>	Selenium	82	<i>fdhC</i> ; selenium metabolism; selenocysteine tRNA	587, 632, 633
<i>semA</i>		40	Sensitivity to microcin E492	884
<i>serA</i>	Serine	63	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)	A, 1100
<i>serB</i>	Serine	100	Phosphoserine phosphatase (EC 3.1.3.3)	A, C, 362, 799
<i>serC</i>	Serine	20	<i>pdxC</i> ; 3-phosphoserine aminotransferase (EC 2.6.1.52)	A, B, 291
<i>serR</i>	Serine	2	Level of seryl-tRNA synthetase	B
<i>serS</i>	Serine	20	Seryl-tRNA synthetase (EC 6.1.1.11)	A, 445
<i>serT</i>	Serine	(22)	<i>divE</i> ; serine tRNA 1	B, 587, 1081
<i>serU</i>	Serine	43	<i>supD, supH, Su-1, sul</i> ; serine tRNA 2	A, C, 587, 1041, 1093
<i>serV</i>	Serine	(58)	Serine tRNA 3	B, 587
<i>serW</i>	Serine	20	Serine tRNA 5 (duplicate gene)	587, 960
<i>serX</i>	Serine	23	Serine tRNA 5 (duplicate gene)	587
<i>sfiC</i>		26	Cell division inhibition; locus of element e14	246, 684, L
<i>shiA</i>	Shikimate	43	Shikimate and dehydrosikimate permease	A
<i>sloB</i>	Slow growth	74	Low growth rate; tolerance to amidinopenicillin and nalidixic acid	B
<i>sodA</i>		88	Superoxide dismutase, manganese	172, 1080, 1109
<i>sodB</i>		36	Superoxide dismutase, iron	171, 172, 415, 798
<i>speA</i>	Spermidine	64	Arginine decarboxylase (EC 4.1.1.19)	A, 127
<i>speB</i>	Spermidine	64	Agmatinase (EC 3.5.3.11)	A, 127
<i>speC</i>	Spermidine	64	Ornithine decarboxylase (EC 4.1.1.17)	A, B, 127
<i>speD</i>	Spermidine	3	S-Adenosylmethionine decarboxylase (EC 4.1.1.50)	B, 1074, 1075
<i>speE</i>	Spermidine	3	Spermidine synthase (putrescine aminopropyltransferase) (EC 2.5.1.16)	1074, 1075
<i>spf</i>		87	“Spot 42” RNA	C, 869
<i>spoT</i>		82	Guanosine 3',5'-bis(diphosphate) 3'-pyrophosphatase	A, B
<i>sppA</i>		39	Protease IV, a signal peptide peptidase	498, 1070
<i>srlA</i>	Sorbitol	58	<i>gutA, sbl</i> ; D-glucitol-specific enzyme II of phosphotransferase system	A, B, C, 1193, 1194
<i>srlB</i>	Sorbitol	58	<i>gutB</i> ; D-glucitol (sorbitol)-specific enzyme III of phosphotransferase system	1193, 1194
<i>srlD</i>	Sorbitol	58	<i>gutD, sbl</i> ; glucitol (sorbitol)-6-phosphate dehydrogenase (EC 1.1.1.140)	A, B, C, 1193, 1194
<i>srlR</i>	Sorbitol	58	Regulatory gene	B, C
<i>srnA</i>		10	Degradation of stable RNA	A
<i>ssaD</i>		9	Suppression of <i>secA</i> mutation	361, 823
<i>ssaE</i>		50	Suppression of <i>secA</i> mutation	361
<i>ssaG</i>		41	Suppression of <i>secA</i> mutation	361
<i>ssaH</i>		94	Suppression of <i>secA</i> mutation	361
<i>ssb</i>	Single-strand binding	92	<i>exrB, lexC</i> ; single-strand DNA-binding protein	B, C
<i>ssp</i>		70	Stringent starvation protein	355, 356, 986
<i>ssr</i>		63	Stable 6S RNA	487, 627
<i>ssyA</i>		54	Suppressor of <i>secY</i> mutation	1000
<i>ssyB</i>		10	Suppressor of <i>secY</i> mutation	1001
<i>ssyD</i>		3	Suppressor of <i>secY</i> mutation	1001
<i>strC</i>	Streptomycin	7	<i>strB</i> ; low-level streptomycin resistance	A
<i>strM</i>	Streptomycin	77	Control of ribosomal ambiguity	A
<i>stsA</i>		84	Altered RNase activity	A
<i>sucA</i>	Succinate	16	<i>lys + met</i> ; succinate requirement; α -ketoglutarate dehydrogenase (decarboxylase component)	A, C, 151, 247, 248, 1174, 1184
<i>sucB</i>	Succinate	16	<i>lys + met</i> ; succinate requirement; α -ketoglutarate dehydrogenase (dihydrolipoyltranssuccinase component)	A, C, 151, 1028, 1029
<i>sucC</i>	Succinate	16	Succinyl-CoA synthetase (EC 6.2.1.5), β subunit	150, 151, 1028, 1029
<i>sucD</i>	Succinate	16	Succinyl-CoA synthetase (EC 6.2.1.5), α subunit	150, 151
<i>suhA</i>		77	Induction of heat shock genes	1099

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Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>sulA</i>		22	<i>sfiA, suf</i> ; suppressor of <i>lon</i>	A, B, 206, 750
<i>sulB</i>		2	See <i>ftsZ</i>	
<i>supB</i>	Suppressor	16	<i>su_B</i> ; suppressor of ochre (UAA) and amber (UAG) mutations; see <i>glnU</i>	
<i>supC</i>	Suppressor	27	<i>su_C, Su-4</i> ; suppressor of ochre (UAA) and amber (UAG) mutations; see <i>tyrT</i>	
<i>supD</i>	Suppressor	43	<i>su_I, Su-1</i> ; suppressor of ochre (UAG) mutations; see <i>serU</i>	
<i>supE</i>	Suppressor	15	<i>su_{II}, Su-2</i> ; suppressor of ochre (UAG) mutations; see <i>glnV</i>	
<i>supF</i>	Suppressor	27	<i>su_{III}, Su-3</i> ; suppressor of amber (UAG) mutations; see <i>tyrT</i>	
<i>supG</i>	Suppressor	17	<i>su-5</i> ; suppressor of ochre (UAA) and amber (UAG) mutations; see <i>lysT</i>	
<i>supH</i>	Suppressor	43	Suppressor; see <i>serU</i>	
<i>supK</i>	Suppressor	62	Suppressor of opal (UGA) mutations; see <i>prfB</i>	
<i>supL</i>	Suppressor	17	<i>su_B</i> ; suppressor of ochre (UAA) and amber (UAG) mutations; see <i>lysT</i>	
<i>supM</i>	Suppressor	90	Suppressor of ochre (UAA) and amber (UAG) mutations, see <i>tyrU</i>	
<i>supN</i>	Suppressor	52	Suppressor of ochre (UAA) and amber (UAG) mutations; see <i>lysV</i>	
<i>supO</i>	Suppressor	27	Suppressor of ochre (UAA) and amber (UAG) mutations; see <i>tyrT</i>	
<i>supP</i>	Suppressor	97	<i>Su-6</i> ; suppressor of amber (UAG) mutations; see <i>leuX</i>	
<i>supQ</i>	Suppressor	13	Suppressor	A
<i>tabC</i>		86	Development of phage T4	B
<i>tag</i>		(72)	3-Methyladenine DNA glycosylase I, constitutive	B, C, 199, 953, 1042
<i>tap</i>		42	Methyl-accepting chemotaxis protein IV	C, 597, 1016, 1017
<i>tar</i>		42	<i>cheM</i> ; methyl-accepting chemotaxis protein II	B, C, 597, 1016, 1017
<i>tdc</i>		68	Threonine dehydratase (EC 4.2.1.16)	252, 388, 389
<i>tdh</i>		81	Threonine dehydrogenase (EC 1.1.1.103)	891, 892
<i>tdi</i>		(4)	Transduction, transformation and rates of mutation	B
<i>tdk</i>		27	Thymidine kinase (EC 2.7.1.75)	A, B
<i>TerA</i>	Terminus	28	DNA replication fork inhibition	267, 343, 460, 463–465, 842, M
<i>TerB</i>	Terminus	36	DNA replication fork inhibition	267, 343, 460, 463–465, 842, M
<i>TerC</i>	Terminus	34	DNA replication fork inhibition	343, 460, M
<i>TerD</i>	Terminus	27	DNA replication fork inhibition	343, 460, M
<i>tesB</i>		10	Thioesterase II	786
<i>tgt</i>		9	tRNA-guanine transglycosylase	C
<i>thdA</i>	Thiophene degradation	11	Utilization of furans and thiophenes; may be <i>tln</i>	2, F
<i>thdC</i>	Thiophene degradation	95	Utilization of furans and thiophenes	2, F
<i>thdD</i>	Thiophene degradation	100	Utilization of furans and thiophenes	2, F
<i>thiA</i>	Thiamin	90	Thiamin thiazole requirement	A
<i>thiB</i>	Thiamin	90	Thiaminphosphate pyrophosphorylase (EC 2.5.1.3)	A
<i>thiC</i>	Thiamin	90	Thiamin pyrimidine requirement	A
<i>thiD</i>	Thiamin	45	Phosphomethylpyrimidine kinase activity	C
<i>thiK</i>	Thiamin	25	Thiamin kinase	C
<i>thiL</i>	Thiamin	10	Thiamin monophosphate kinase	C
<i>thrA</i>	Threonine	0	<i>HS, thrD</i> ; aspartokinase I-homoserine dehydrogenase I (EC 2.3.2.4–EC 1.1.1.3)	A, B, C, 244, 678
<i>thrB</i>	Threonine	0	Homoserine kinase (EC 2.7.1.39)	A, C, 948
<i>thrC</i>	Threonine	0	Threonine synthase (EC 4.2.99.2)	A, C, 836
<i>thrS</i>	Threonine	38	Threonyl-tRNA synthetase (EC 6.1.1.3)	B, C, 717, 867, 878, 1034, 1170, 1190
<i>thrT</i>	Threonine	90	Threonine tRNA 3	A, B, C, 587
<i>thrU</i>	Threonine	90	Threonine tRNA 4	B, C, 587
<i>thrV</i>	Threonine	72	Threonine tRNA 1; at distal end of <i>rrnD</i> operon	C, 214, 587
<i>thrW</i>	Threonine	6	Threonine tRNA 2	214, 242, 587
<i>thyA</i>	Thymine	61	Thymidylate synthetase (EC 2.1.1.45)	A, C, 83, 296, 965
<i>tkt</i>		(62)	Transketolase (EC 2.2.1.1)	A
<i>tlnA</i>		11	<i>tlnI</i> ; resistance or sensitivity to thiolitin	C
<i>tmk</i>		25	Deoxythymidine kinase	96, 257
<i>tmaA</i>		84	<i>ind, tnaR</i> ; tryptophanase (EC 4.1.99.1)	A, B, C, 1045

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Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>tnm</i>		92	Transposition of Tn9 and other transposons; development of phage Mu	C
<i>toc</i>		67	Compensation for loss of DNA topoisomerase I	886
<i>tolA</i>	Tolerance	17	<i>cim</i> , <i>excC</i> , <i>lky</i> , <i>tol-2</i> ; tolerance to group A colicins and single-stranded filamentous DNA phage	A, 337, 1061, 1062, V
<i>tolB</i>	Tolerance	17	<i>tol-3</i> ; tolerance to colicins E2, E3, A, and K	A, 337, 624, 625, 1061, 1062, V
<i>tolC</i>	Tolerance	66	<i>colEl-i</i> , <i>mtcB</i> , <i>refI</i> , <i>tol-8</i> ; specific tolerance to colicin E1, expression of outer membrane proteins	A, C, 425, 426, 826
<i>tolD</i>	Tolerance	(23)	Tolerance to colicins E2 and E3; ampicillin resistance	A
<i>tolE</i>	Tolerance	(23)	Tolerance to colicins E2 and E3; ampicillin resistance	A
<i>tolI</i>	Tolerance	(0)	Tolerance to colicins Ia and Ib	A
<i>tolJ</i>	Tolerance	0	Resistance to colicins L, A, and S4; partial resistance to colicins E and K	B
<i>tolM</i>	Tolerance	72	<i>cmt</i> ; high-level tolerance to colicin M	C, 432, 730
<i>tolQ</i>	Tolerance	17	<i>fii</i> , <i>tolP?</i> ; tolerance to group A colicins and single-stranded filamentous DNA phage	1061, 1062, V
<i>tolR</i>	Tolerance	17	Tolerance to group A colicins and single-stranded filamentous DNA phage	1062, V
<i>tolZ</i>	Tolerance	77	Tolerance to colicins E2, E3, D, Ia, and Ib; generation of chemical proton gradient	715
<i>tonA</i>	T-one	4	See <i>fhuA</i>	
<i>tonB</i>	T-one	28	<i>exbA</i> , <i>Tlrec</i> ; uptake of chelated iron and cyanobalimin; sensitivity to phages T1 and φ80 and colicins	A, B, C, 874, 875
<i>topA</i>	Topoisomerase	28	<i>supX</i> ; DNA topoisomerase I, ω protein	C, 704, 825, 1115, 1154
<i>torA</i>		28	Trimethylamine N-oxide reductase	837
<i>tpiA</i>		89	Triosephosphate isomerase (EC 5.3.1.1)	A, B, 456, 849
<i>tpr</i>		27	A protaminelike protein	C
<i>treA</i>	Trehalose	26	Trehalase, periplasmic	B, 116, 730
<i>trg</i>		31	Methyl-accepting chemotaxis protein III	B, C, 113, 441
<i>trkA</i>		72	Transport of potassium	A, 432, 730
<i>trkB</i>		73	See <i>kefB</i>	
<i>trkC</i>		1	See <i>kefB</i>	
<i>trkD</i>		84	Transport of potassium	A, B, C
<i>trkE</i>		29	Transport of potassium	A
<i>trmA</i>	tRNA methyltransferase	90	tRNA (uracil-5)-methyltransferase (EC 2.1.1.35)	A, B, C, 654
<i>trmB</i>	tRNA methyltransferase	(7)	tRNA (guanine-7)-methyltransferase (EC 2.1.1.33)	A
<i>trmC</i>	tRNA methyltransferase	(56)	5-Methylaminoethyl-2-thiouridine in tRNA	A, B, 428
<i>trmD</i>	tRNA methyltransferase	(57)	tRNA (guanine-7)-methyltransferase (EC 2.1.1.31)	B, 162-164
<i>trmE</i>	tRNA methyltransferase	84	<i>asuE?</i> ; 5-methylaminoethyl-2-thiouridine biosynthesis	307
<i>trmF</i>	tRNA methyltransferase	84	5-methylaminoethyl-2-thiouridine biosynthesis	307
<i>trnA</i>		59	<i>glnU</i> ; level of several tRNAs	C
<i>trpA</i>	Tryptophan	28	<i>tryp-2</i> ; tryptophan synthase (EC 4.2.1.20), A protein	A, B, C
<i>trpB</i>	Tryptophan	28	<i>tryp-1</i> ; tryptophan synthase (EC 4.2.1.20), B protein	A, C
<i>trpC</i>	Tryptophan	28	<i>tryp-3</i> ; <i>N</i> -(5-phosphoribosyl)anthranilate isomerase indole-3-glycerol phosphate synthetase	A, B, C
<i>trpD</i>	Tryptophan	28	<i>tryE</i> ; glutamine amidotransferase-phosphoribosyl anthranilate transferase	A, C
<i>trpE</i>	Tryptophan	28	<i>anth</i> , <i>tryp-4</i> , <i>tryD</i> ; anthranilate synthase (EC 4.1.3.27)	A, B, C
<i>trpP</i>	Tryptophan	84	Low-affinity tryptophan-specific permease	C
<i>trpR</i>	Tryptophan	100	<i>Rtry</i> ; regulation of <i>trp</i> operon and <i>aroH</i> ; <i>trp</i> aporepressor	A, B, C
<i>trpS</i>	Tryptophan	74	Tryptophanyl-tRNA synthetase (EC 6.1.1.2)	A, B, C
<i>trpT</i>	Tryptophan	85	<i>su7</i> , <i>su8</i> , <i>su9</i> , <i>supU</i> , <i>supV</i> ; tryptophan tRNA gene at distal end of <i>rrnC</i> operon	A, B, C, 587
<i>trxA</i>	Thioredoxin	86	<i>fip</i> , <i>tsnC</i> ; thioredoxin	B, 14, 649, 650, 713, 935, 936, 938, 1153
<i>trxB</i>	Thioredoxin	21	Thioredoxin reductase	431, 937, 939
<i>tsf</i>		4	Protein chain elongation factor, EF-Ts	B, C
<i>tsr</i>		99	<i>cheD</i> ; methyl-accepting chemotaxis protein I	B, C, 126, 169
<i>tsx</i>	T-six	9	<i>nupA</i> , <i>T6rec</i> ; nucleoside uptake; receptor for phage T6 and colicin K	A, B, 130
<i>tufA</i>		74	Protein chain elongation factor; EF-Tu (duplicate gene)	A, B, C
<i>tufB</i>		90	Protein chain elongation factor; EF-Tu (duplicate gene)	A, B, C, 1079
<i>tus</i>		36	DNA-binding protein; inhibition of replication at <i>Ter</i> sites	C, 464, 466, 842, M
<i>tynA</i>		(27)	Tyramine oxidase (EC 1.4.3.4)	B

Continued on following page

TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>tyrA</i>	Tyrosine	57	Chorismate mutase T (EC 5.4.99.5)—prephenate dehydrogenase (EC 1.3.1.12)	A, 488
<i>tyrB</i>	Tyrosine	92	Tyrosine aminotransferase (EC 2.6.1.5), tyrosine repressive	B, 340, 605, 1200
<i>tyrP</i>	Tyrosine	42	Tyrosine-specific transport system	C, 558, 559, 1186
<i>tyrR</i>	Tyrosine	29	Regulation of <i>aroF</i> , <i>aroG</i> , and <i>tyrA</i> and aromatic amino acid transport systems	A, B, C, 217, 218
<i>tyrS</i>	Tyrosine	36	Tyrosyl-tRNA synthetase (EC 6.1.1.1)	A, B, C, 67
<i>tyrT</i>	Tyrosine	27	<i>sulIII</i> , <i>Su-3</i> , <i>su_c</i> , <i>Su-4</i> , <i>supF</i> , <i>supE</i> , <i>tyrV</i> ; tyrosine tRNA 1 (tandemly duplicated gene)	A, B, C, 587
<i>tyrU</i>	Tyrosine	90	<i>supM</i> ; tyrosine tRNA 2	A, B, C, 587
<i>ubiA</i>	Ubiquinone	92	4-Hydroxybenzoate → 3-octaprenyl 4-hydroxybenzoate	A, C
<i>ubiB</i>	Ubiquinone	87	2-Octaprenylphenol → 2-octaprenyl-6-methoxyphenol	A
<i>ubiC</i>	Ubiquinone	92	Chorismate lyase	A
<i>ubiD</i>	Ubiquinone	87	3-Octaprenyl-4-hydroxybenzoate → 2-octaprenylphenol	A
<i>ubiE</i>	Ubiquinone	87	2-Octaprenyl-6-methoxy-1,4-benzoquinone → 2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinone	A
<i>ubiF</i>	Ubiquinone	15	2-Octaprenyl-3-methyl-6-methoxy-1,4-benzoquinone → 2-octaprenyl-3-methyl-5-hydroxy-6-methoxy-1,4-benzoquinone	A
<i>ubiG</i>	Ubiquinone	48	2-Octaprenyl-3-methyl-5-hydroxy-6-methoxy-1,4-benzoquinone → ubiquinone 8	A, B, C, 375
<i>ubiH</i>	Ubiquinone	63	2-Octaprenyl-6-methoxyphenol → 2-octaprenyl-6-methoxy-1,4-benzoquinone	A
<i>ubiX</i>	Ubiquinone	50	Sequence homologous to <i>ubiX</i> of <i>S. typhimurium</i> , which codes for polypropenyl <i>p</i> -hydroxybenzoate carboxylase	807
<i>udk</i>		45	Uridine kinase (EC 2.7.1.48)	A, C
<i>udp</i>		86	Uridine phosphorylase (EC 2.4.2.3)	A, 14, 15
<i>ugpA</i>		76	<i>sn</i> -Glycerol-3-phosphate transport system	A, 828, 977, 978
<i>ugpB</i>		76	<i>sn</i> -Glycerol-3-phosphate transport system; periplasmic binding protein	C, 828, 977, 978
<i>ugpC</i>		76	<i>sn</i> -Glycerol-3-phosphate transport system	828, 977, 978
<i>ugpE</i>		76	<i>sn</i> -Glycerol-3-phosphate transport system, membrane protein	828, 977, 978
<i>uhpA</i>		82	Positive activator of <i>uhpt</i> transcription	352, 543, 993, 1172
<i>uhpB</i>		82	Regulatory gene	352, 1172
<i>uhpC</i>		82	Regulatory gene	A, B, C, 352, 543, 993, 1172
<i>uhpR</i>		82	Regulation of hexose phosphate transport; possibly outer membrane receptor for glucose 6-phosphate	A, B, C
<i>uhpT</i>		82	Transport of hexose phosphates, transport protein	A, B, C, 352, 543, 993, 1172
<i>uidA</i>		36	<i>gurA</i> ; β-D-glucuronidase (EC 3.2.1.31)	A, B, C, 107, 527
<i>uidR</i>		36	Regulatory gene	A, B, C, 105, 107, 108
<i>umuC</i>		26	<i>uvr</i> , induction of mutations by UV; error-prone repair	B, 137, 259, 305, 570, 706, 843, 1005
<i>umuD</i>		26	<i>uvr</i> ; inducible mutagenesis; error-prone repair	C, 259, 305, 570, 706, 843, 1005
<i>unc</i>			See <i>atp</i>	
<i>ung</i>		56	Uracil-DNA-glycosylase	B, 1142
<i>upp</i>		54	<i>uraP</i> ; uracil phosphoribosyltransferase (EC 2.4.2.9)	A, B, 476
<i>ups</i>		26	Efficiency of nonsense suppressors	B, 941
<i>ushA</i>		11	UDP-glucose hydrolase (F'-nucleotidase)	A, B, C, 155
<i>uup</i>		21	Precise excision of insertion elements	476
<i>uvrA</i>	Ultraviolet	92	<i>dar</i> ; repair of UV damage to DNA; excision nuclease	A, B, C, 496
<i>uvrB</i>	Ultraviolet	18	<i>dar-1,6</i> ; DNA repair; excision nuclease	A, B, C, 26, 47, 1072
<i>uvrC</i>	Ultraviolet	42	<i>dar-4,5</i> ; repair of UV damage to DNA; excision nuclease	A, C, 338, 339, 956, 991, 992, 1140
<i>uvrD</i>	Ultraviolet	86	<i>dar-2</i> , <i>dda</i> , <i>mutU</i> , <i>pdeB</i> , <i>recL</i> , <i>uvrE</i> , <i>uvr502</i> ; DNA-dependent ATPase I and DNA helicase II	A, B, C, 14, 33, 297, 326, 327, 459, 603, 1083, 1198
<i>uxaA</i>		68	Altronate hydrolase (EC 4.2.1.7)	A, B, C
<i>uxaB</i>		(52)	Altronate oxidoreductase (EC 1.1.1.58)	A, B, 103, 104, 490, 711
<i>uxaC</i>		68	Uronate isomerase (EC 5.3.1.12)	A, B, C, 102, 710, 711
<i>uxuA</i>		98	Mannanose hydrolase (EC 4.2.1.8)	A, B, C, 106, 347
<i>uxuB</i>		98	Mannanose oxidoreductase (EC 1.1.1.57)	A, B, C, 106, 347

Continued on following page

TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>uxuR</i>		98	Regulatory gene for <i>uxuBA</i> operon	B, C
<i>valS</i>	Valine	97	<i>val-act</i> ; valyl-tRNA synthetase (EC 6.1.1.9)	A, B, C, 443, 451, 452, 1015
<i>valT</i>	Valine	17	Valine tRNA 1	B, C, 587, 1211
<i>valU</i>		52	Valine tRNA 1 (tandemly triplicated gene)	587, D
<i>valV</i>		37	Valine tRNA 2B	587
<i>valW</i>		37	Valine tRNA 2A	587
<i>weeA</i>		67	Cell elongation	265
<i>xapA</i>		52	<i>pndA</i> ; xanthosine phosphorylase	C, 582
<i>xapR</i>		52	<i>pndR</i> ; regulatory gene	C, 582
<i>xthA</i>		38	Exonuclease III	A, B, C
<i>xseA</i>		54	Exonuclease VII, large subunit	B, 187, 1131
<i>xseB</i>		10	Exonuclease VII, small subunit	1131, 1132
<i>xylA</i>	Xylose	80	D-Xylose isomerase (EC 5.3.1.5)	A, C, 132, 610, 923, 970
<i>xylB</i>	Xylose	80	Xylulokinase (EC 2.7.1.17)	A, C, 132, 923
<i>xylE</i>	Xylose	91	Xylose-proton symport	255, 256, 344, 609
<i>xylF</i>	Xylose	80	<i>xylT</i> ; xylose binding protein transport system	256, 610, 923
<i>xylR</i>	Xylose	80	Regulatory gene	A, C, 923
<i>zwf</i>	Zwischenferment	41	Glucose-6-phosphate dehydrogenase (EC 1.1.1.49)	A

^a Numbers refer to the time scale shown in Fig. 1. Parentheses indicate approximate map locations.^b Abbreviations: CoA, coenzyme A; DCCD, N,N'-dicyclohexylcarbodiimide; NEM, N-ethylmaleimide.^c Numbers refer to Literature Cited. Letters refer to: (A) literature cited in Table 2 of reference 46; (B) literature cited in Table 1 of reference 45; (C) literature cited in Table 1 of reference 43; and personal communications from (D) Y. Brun, (E) K. Burton, (F) D. Clark, (G) J. Coleman, (H) S. Ferro-Novick, J. Sands, and J. Beckwith, (I) J. Gowrishankar, (J) B. G. Hall, (K) K. Hantke, (L) C. W. Hill, (M) P. Kuempel, (N) I. G. Old, (O) D. B. Oliver, (P) D. Oxender, (Q) R. Plapp, (R) P. Rabinovich, (S) J. M. Smith, (T) M. Volkert, (U) B. Wanner, (V) R. Webster, and (W) B. Weiss

TABLE 2. Alternate gene symbols

Alternate symbol	Symbol in Table 1	Alternate symbol	Symbol in Table 1
<i>acrB</i>	<i>gyrB</i>	<i>bisA</i>	<i>chlA</i>
<i>ade</i>	<i>pur</i>	<i>bisB</i>	<i>chlE</i>
<i>adth_a</i>	<i>purD</i>	<i>bisD</i>	<i>narG</i>
<i>adth_b</i>	<i>purG</i>	<i>blu</i>	<i>pgl, pgm, malP</i>
<i>aidA</i>	<i>alkA</i>	<i>brnP</i>	<i>ilvH</i>
<i>aidD</i>	<i>alkB</i>	<i>cap</i>	<i>car, crp</i>
<i>ala-act</i>	<i>alaS</i>	<i>capR</i>	<i>lon</i>
<i>ald</i>	<i>fba</i>	<i>car</i>	<i>ptsG</i>
<i>alnA</i>	<i>dadB</i>	<i>cat</i>	<i>ptsG</i>
<i>alnR</i>	<i>dadQ</i>	<i>cbr</i>	<i>fep</i>
<i>alt</i>	<i>rpoD</i>	<i>cbt</i>	<i>fep</i>
<i>amk</i>	<i>nek</i>	<i>cer</i>	<i>btuB</i>
<i>ampA</i>	<i>ampC</i>	<i>cheC</i>	<i>flaA</i>
<i>anth</i>	<i>trpE</i>	<i>cheD</i>	<i>tsr</i>
<i>apk</i>	<i>lysC</i>	<i>cheM</i>	<i>tar</i>
<i>arg + ura</i>	<i>car</i>	<i>cheX</i>	<i>cheR</i>
<i>aroR</i>	<i>aroT</i>	<i>chlC</i>	<i>narG, narH</i>
<i>asp</i>	<i>ppc</i>	<i>chlG</i>	<i>narG</i>
<i>aspB</i>	<i>gltB</i>	<i>chlI</i>	<i>narI</i>
<i>asuC</i>	<i>hisT</i>	<i>cim</i>	<i>tolA</i>
<i>asuD</i>	<i>lysS</i>	<i>cmlB</i>	<i>ompF</i>
<i>ata</i>	<i>attP22</i>	<i>cmt</i>	<i>tolM</i>
<i>att82, att434</i>	<i>atty</i>	<i>coa</i>	<i>ompF</i>
<i>azi</i>	<i>secA</i>	<i>coleI-i</i>	<i>tolC</i>
<i>bfe</i>	<i>btuB</i>	<i>con</i>	<i>ompA, rfa</i>
<i>bglY</i>	<i>osmZ</i>	<i>cop</i>	<i>het</i>
<i>bioR</i>	<i>birA</i>	<i>Cou</i>	<i>gyrB</i>
<i>birB (bir)</i>	<i>bioP</i>	<i>cqsA</i>	<i>rRNA</i>

Continued on following page

TABLE 2—Continued

Alternate symbol	Symbol in Table 1	Alternate symbol	Symbol in Table 1
<i>mtcA</i>	<i>acrA</i>	<i>psuA</i>	<i>rho</i>
<i>mtcB</i>	<i>tolC</i>	<i>ptsF</i>	<i>fruA</i>
<i>muc</i>	<i>lon</i>	<i>ptsL</i>	<i>manX</i>
<i>mutD</i>	<i>dnaQ</i>	<i>ptsM</i>	<i>manX,Y,Z</i>
<i>mutR</i>	<i>mutH</i>	<i>ptsN</i>	<i>nagE</i>
<i>mutU</i>	<i>uvrD</i>	<i>ptsP</i>	<i>manY</i>
<i>nalA</i>	<i>gyrA</i>	<i>ptsX</i>	<i>manX,Y,Z</i>
<i>nalC,D</i>	<i>gyrB</i>	<i>pup</i>	<i>deoD</i>
<i>nam</i>	<i>pncA</i>	<i>pyrA</i>	<i>car</i>
<i>ncf</i>	<i>hemB</i>	<i>rad</i>	<i>uvrD</i>
<i>neaA</i>	<i>rpsQ</i>	<i>radB</i>	<i>recN</i>
<i>nic</i>	<i>nad</i>	<i>ramA</i>	<i>rpsD</i>
<i>nirA</i>	<i>fnr</i>	<i>ramB</i>	<i>rimG</i>
<i>nirR</i>	<i>fnr</i>	<i>RC</i>	<i>rel</i>
<i>nitA</i>	<i>rho</i>	<i>recL</i>	<i>uvrD</i>
<i>nitB</i>	<i>rpoB</i>	<i>refI</i>	<i>tolC</i>
<i>nmpA</i>	<i>pst, phoS,T</i>	<i>refII</i>	<i>cet</i>
<i>nmpB</i>	<i>phoR</i>	<i>relC</i>	<i>rplK</i>
<i>ntrA</i>	<i>rpoN</i>	<i>res</i>	<i>rimF</i>
<i>ntrB</i>	<i>glnL</i>	<i>resA</i>	<i>polA</i>
<i>ntrC</i>	<i>glnG</i>	<i>rglA</i>	<i>mcra</i>
<i>nucR</i>	<i>deoR</i>	<i>rglB</i>	<i>mcrB</i>
<i>nupA</i>	<i>tsx</i>	<i>rif</i>	<i>rpoB</i>
<i>nusE</i>	<i>rpsJ</i>	<i>rimA</i>	<i>rpmH</i>
<i>old</i>	<i>fad</i>	<i>rm</i>	<i>hsd</i>
<i>ole</i>	<i>fadR</i>	<i>rnsA</i>	<i>rna</i>
<i>ompB</i>	<i>envZ, ompR</i>	<i>rnsC</i>	<i>rho</i>
<i>ompE</i>	<i>phoE</i>	<i>rodA</i>	<i>mrdB</i>
<i>osrA</i>	<i>proU</i>	<i>rodY</i>	<i>envB</i>
<i>par</i>	<i>ompC</i>	<i>ron</i>	<i>rpoB</i>
<i>paxA</i>	<i>dcd</i>	<i>rorA</i>	<i>recB</i>
<i>pbpA</i>	<i>mrdA</i>	<i>rpx</i>	<i>rps</i>
<i>pbpB</i>	<i>ftsI</i>	<i>rpy</i>	<i>rpl</i>
<i>pbpF</i>	<i>mrcB</i>	<i>rpz</i>	<i>rpm</i>
<i>pcbA</i>	<i>gyrB</i>	<i>sbcA</i>	<i>rac</i>
<i>pdeB</i>	<i>uvrD</i>	<i>sbl</i>	<i>srl</i>
<i>pdeC</i>	<i>lig</i>	<i>sdrA</i>	<i>rnh</i>
<i>pdxC</i>	<i>serC</i>	<i>sec</i>	<i>hemF</i>
<i>pdxF</i>	<i>serC</i>	<i>secC</i>	<i>rpsO</i>
<i>pdzA</i>	<i>rplT</i>	<i>secY</i>	<i>prlA</i>
<i>pea</i>	<i>secA</i>	<i>seg</i>	<i>arcA</i>
<i>pel</i>	<i>manY</i>	<i>Sep</i>	<i>ftsI</i>
<i>perA</i>	<i>envZ</i>	<i>sez</i>	<i>rpoA</i>
<i>pfv</i>	<i>dacA</i>	<i>sfiA</i>	<i>sulA</i>
<i>pgsB</i>	<i>lpxB</i>	<i>sfiB</i>	<i>ftsZ</i>
<i>phe-act</i>	<i>pheS</i>	<i>sfrA</i>	<i>arcA</i>
<i>phoS</i>	<i>pstS</i>	<i>sfrB</i>	<i>rfaH</i>
<i>phoT</i>	<i>pstA,B, phoU</i>	<i>sin</i>	<i>rnh</i>
<i>phoW</i>	<i>pstC</i>	<i>skp</i>	<i>hlpA</i>
<i>phs</i>	<i>rpoA</i>	<i>sof</i>	<i>dut</i>
<i>phx</i>	<i>rfa</i>	<i>som</i>	<i>rfb</i>
<i>pil</i>	<i>fim</i>	<i>spcA</i>	<i>rpsE</i>
<i>plsA</i>	<i>adk</i>	<i>spr</i>	<i>lexA</i>
<i>PMG</i>	<i>mgl</i>	<i>ssd</i>	<i>ecfB</i>
<i>pmi</i>	<i>manA</i>	<i>ssyF</i>	<i>rpsA</i>
<i>pndA</i>	<i>xapA</i>	<i>ssyG</i>	<i>infB</i>
<i>pndR</i>	<i>xapR</i>	<i>stc</i>	<i>micF</i>
<i>poaA</i>	<i>putA</i>	<i>stl</i>	<i>rpoB</i>
<i>pol</i>	<i>oriC</i>	<i>strA</i>	<i>rpsL</i>
<i>polC</i>	<i>dnaE</i>	<i>stsB</i>	<i>rimH</i>
<i>pon</i>	<i>lpcB, mrc</i>	<i>stv</i>	<i>rpoB</i>
<i>popA</i>	<i>hemH</i>	<i>Su, su</i>	<i>sup</i>
<i>popB</i>	<i>hemF</i>	<i>suβ</i>	<i>lysTβ</i>
<i>popE</i>	<i>hemC</i>	<i>sud₂</i>	<i>rpsD</i>
<i>prd</i>	<i>fuc</i>	<i>sueB</i>	<i>prfA</i>
<i>prv</i>	<i>mutH</i>	<i>sufD</i>	<i>glyU</i>
<i>psiB</i>	<i>ugpA,B</i>	<i>sulB</i>	<i>ftsZ</i>
<i>psiC</i>	<i>ugpA,B</i>	<i>sumA</i>	<i>glyT</i>
<i>psiD</i>	<i>phnD</i>	<i>sumB</i>	<i>glyU</i>

Continued on following page

TABLE 2—Continued

Alternate symbol	Symbol in Table 1	Alternate symbol	Symbol in Table 1
<i>cqsB</i>	. <i>rrnC</i>	<i>gpp</i>	. <i>gpt</i>
<i>cqsD</i>	. <i>rrnD</i>	<i>gpt</i>	. <i>ptsG</i>
<i>CR</i>	. <i>ptsG</i>	<i>gptB</i>	. <i>manX,Z</i>
<i>cru</i>	. <i>nupC</i>	<i>groE</i>	. <i>mop</i>
<i>cry</i>	. <i>ompR, ompF</i>	<i>groN</i>	. <i>rpoB</i>
<i>csm</i>	. <i>crp</i>	<i>groP</i>	. <i>dnaB, dnaJ, dnaK</i>
<i>ctr</i>	. <i>ptsH, ptsI</i>	<i>grpA</i>	. <i>dnaB</i>
<i>cur</i>	. <i>osmZ</i>	<i>grpC</i>	. <i>dnaJ, dnaK</i>
<i>cxr</i>	. <i>cxm</i>	<i>grpF</i>	. <i>dnaK</i>
<i>cybA</i>	. <i>sdhC</i>	<i>gts</i>	. <i>qmeA</i>
<i>dagA</i>	. <i>cycA</i>	<i>gura</i>	. <i>uidA</i>
<i>dap + hom</i>	. <i>asd</i>	<i>gut</i>	. <i>srl</i>
<i>dar</i>	. <i>uvr</i>	<i>gxu</i>	. <i>gpt</i>
<i>dasC</i>	. <i>rep?</i>	<i>H</i>	. <i>fliC</i>
<i>dasF</i>	. <i>rnh</i>	<i>hag</i>	. <i>fliC</i>
<i>dda</i>	. <i>uvrD</i>	<i>hdh</i>	. <i>mop</i>
<i>deg</i>	. <i>lon</i>	<i>herA</i>	. <i>rnh</i>
<i>dhbB</i>	. <i>bioR</i>	<i>hid</i>	. <i>himA</i>
<i>dhl</i>	. <i>lpd</i>	<i>himB</i>	. <i>gyrB</i>
<i>dir</i>	. <i>lon</i>	<i>hin</i>	. <i>rpoH</i>
<i>divA</i>	. <i>ftsA</i>	<i>hip</i>	. <i>himD</i>
<i>divE</i>	. <i>serT</i>	<i>Hpr</i>	. <i>ptsH</i>
<i>dnaF</i>	. <i>nrdA</i>	<i>hrbA</i>	. <i>brnQ</i>
<i>dnaL</i>	. <i>lig</i>	<i>hrbB,C,D</i>	. <i>livG,H,J,K</i>
<i>dnaS</i>	. <i>dut</i>	<i>hs</i>	. <i>hsd</i>
<i>dnaW</i>	. <i>adk</i>	<i>Hs</i>	. <i>thrA</i>
<i>dnaY</i>	. <i>argU</i>	<i>hsm</i>	. <i>hsdM</i>
<i>dra</i>	. <i>deoC</i>	<i>hsp</i>	. <i>hsd</i>
<i>drm</i>	. <i>deoB</i>	<i>hsr</i>	. <i>hsdR</i>
<i>dye</i>	. <i>arcA</i>	<i>hss</i>	. <i>hsdS</i>
<i>eps</i>	. <i>rpsE</i>	<i>htpR</i>	. <i>rpoH</i>
<i>eryA</i>	. <i>rplD</i>	<i>icl</i>	. <i>aceA</i>
<i>eryB</i>	. <i>rplV</i>	<i>ile</i>	. <i>ilvA</i>
<i>eup</i>	. <i>ecfB</i>	<i>ind</i>	. <i>tnaA</i>
<i>extA</i>	. <i>tonB</i>	<i>ins</i>	. <i>glyV, glyW</i>
<i>excC</i>	. <i>tolA</i>	<i>K12</i>	. <i>rpsG</i>
<i>exrA</i>	. <i>lexA</i>	<i>kac</i>	. <i>kdp</i>
<i>exrB</i>	. <i>ssb</i>	<i>kdga</i>	. <i>eda</i>
<i>fabC</i>	. <i>fabB</i>	<i>kga</i>	. <i>eda</i>
<i>fam</i>	. <i>rpoH</i>	<i>kim</i>	. <i>qin</i>
<i>far</i>	. <i>fusA</i>	<i>kmt</i>	. <i>ompB</i>
<i>fda</i>	. <i>fba</i>	<i>lcs</i>	. <i>asnS</i>
<i>fdhA</i>	. <i>selA, selB</i>	<i>ldh</i>	. <i>dld</i>
<i>fdhB</i>	. <i>selD</i>	<i>leuK</i>	. <i>hisT</i>
<i>fdhC</i>	. <i>selC</i>	<i>leuX</i>	. <i>leuSo, leuSp</i>
<i>fdp</i>	. <i>fbp</i>	<i>lexB</i>	. <i>recA</i>
<i>feuA</i>	. <i>cir</i>	<i>lexC</i>	. <i>ssb</i>
<i>feuB</i>	. <i>sep</i>	<i>lir</i>	. <i>acra</i>
<i>fexA</i>	. <i>arcA</i>	<i>lky</i>	. <i>tolB</i>
<i>fii</i>	. <i>tolQ, tolR</i>	<i>lop</i>	. <i>ligA</i>
<i>fipA</i>	. <i>trxA</i>	<i>loxB</i>	. <i>attP1,P7</i>
<i>fit</i>	. <i>infC</i>	<i>lps</i>	. <i>rfa</i>
<i>fla</i>	. <i>flg, fli, fli</i>	<i>lss</i>	. <i>livR</i>
<i>flaJ</i>	. <i>motA, motB</i>	<i>lstR</i>	. <i>livR</i>
<i>flaF</i>	. <i>fliC</i>	<i>lys + met</i>	. <i>sucA, sucB</i>
<i>flb</i>	. <i>flg, fli, fli</i>	<i>lysP</i>	. <i>cadR</i>
<i>fliA</i>	. <i>ileR?</i>	<i>mas</i>	. <i>aceB</i>
<i>fpk</i>	. <i>fruK</i>	<i>Mb</i>	. <i>acra</i>
<i>fpr</i>	. <i>fruF</i>	<i>mbl</i>	. <i>acra</i>
<i>frdB</i>	. <i>fnr</i>	<i>mec</i>	. <i>dcm</i>
<i>ftsB</i>	. <i>nrdB</i>	<i>meoA</i>	. <i>ompC</i>
<i>gad</i>	. <i>gap</i>	<i>mlpA</i>	. <i>lpp</i>
<i>glmD</i>	. <i>nagB</i>	<i>mni</i>	. <i>manC</i>
<i>glnF</i>	. <i>rpoN</i>	<i>molA</i>	. <i>malM</i>
<i>gltC</i>	. <i>gltSo</i>	<i>mon</i>	. <i>envB</i>
<i>glu</i>	. <i>ppc</i>	<i>motD</i>	. <i>fliN</i>
<i>glut</i>	. <i>gltA</i>	<i>mpt</i>	. <i>manX,Z</i>
<i>gly-act</i>	. <i>glyS</i>	<i>mra</i>	. <i>murF</i>
<i>glyD</i>	. <i>gpt</i>	<i>msp</i>	. <i>arcA</i>

Continued on following page

TABLE 2—Continued

Alternate symbol	Symbol in Table 1	Alternate symbol	Symbol in Table 1
<i>sun</i>	<i>rho</i>	<i>tpp</i>	<i>deoA</i>
<i>sup_{s20}</i>	<i>rpsT</i>	<i>tre</i>	<i>Ter</i>
<i>supK</i>	<i>prfB</i>	<i>trkB</i>	<i>kefB</i>
<i>T1rec</i>	<i>tonB</i>	<i>trkC</i>	<i>kefC</i>
<i>T1, T5rec</i>	<i>fhuA</i>	<i>trpP</i>	<i>aroT</i>
<i>T6rec</i>	<i>tsx</i>	<i>try</i>	<i>trp</i>
<i>tabB</i>	<i>mop</i>	<i>tryp</i>	<i>trp</i>
<i>tabD</i>	<i>rpoB, rpoC</i>	<i>ts-9</i>	<i>rts</i>
<i>talA</i>	<i>alaT</i>	<i>tsl</i>	<i>lexA</i>
<i>talD</i>	<i>alaU</i>	<i>tsnC</i>	<i>trxA</i>
<i>tasC</i>	<i>aspT</i>	<i>tsu</i>	<i>rho</i>
<i>tfrA</i>	<i>lpcA</i>	<i>tss</i>	<i>asns</i>
<i>tgl</i>	<i>ptsG</i>	<i>ttr</i>	<i>fadL</i>
<i>tgs</i>	<i>crr?</i>	<i>tut</i>	<i>ompA</i>
<i>tgtB</i>	<i>gltT</i>	<i>uar</i>	<i>prfA</i>
<i>tgtC</i>	<i>gltU</i>	<i>umg</i>	<i>ptsG</i>
<i>tgtE</i>	<i>gltV</i>	<i>umuA</i>	<i>lexA</i>
<i>thdB</i>	<i>fadR</i>	<i>umuB</i>	<i>recA</i>
<i>thyR</i>	<i>deoB, deoC</i>	<i>unc</i>	<i>atp</i>
<i>tif</i>	<i>recA</i>	<i>uraP</i>	<i>upp</i>
<i>tmr</i>	<i>fol</i>	<i>usgA</i>	<i>gntT</i>
<i>tolF</i>	<i>ompF</i>	<i>uvrM</i>	<i>umu</i>
<i>tolG</i>	<i>ompA</i>	<i>uvrF</i>	<i>recF</i>
<i>tolP</i>	<i>tolQ</i>	<i>val-act</i>	<i>vals</i>
<i>tonA</i>	<i>fhuA</i>	<i>vtr</i>	<i>fabF</i>
<i>TP</i>	<i>deoA</i>	<i>xonA</i>	<i>sbcB</i>
<i>tpo</i>	<i>envZ</i>	<i>zab</i>	<i>recA</i>

although the relative positions of some genes have been determined precisely.

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